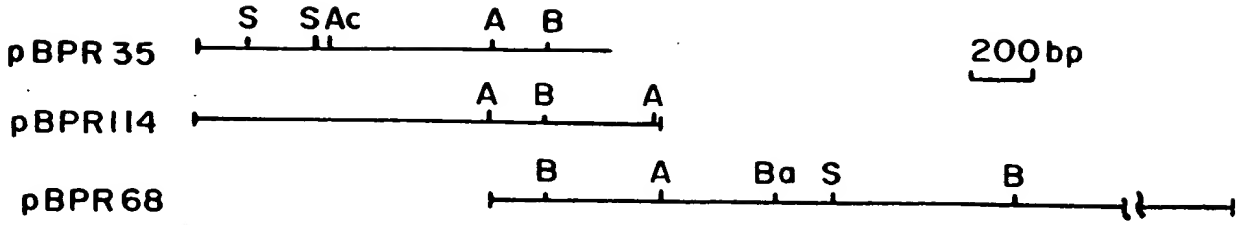


FIG. 1

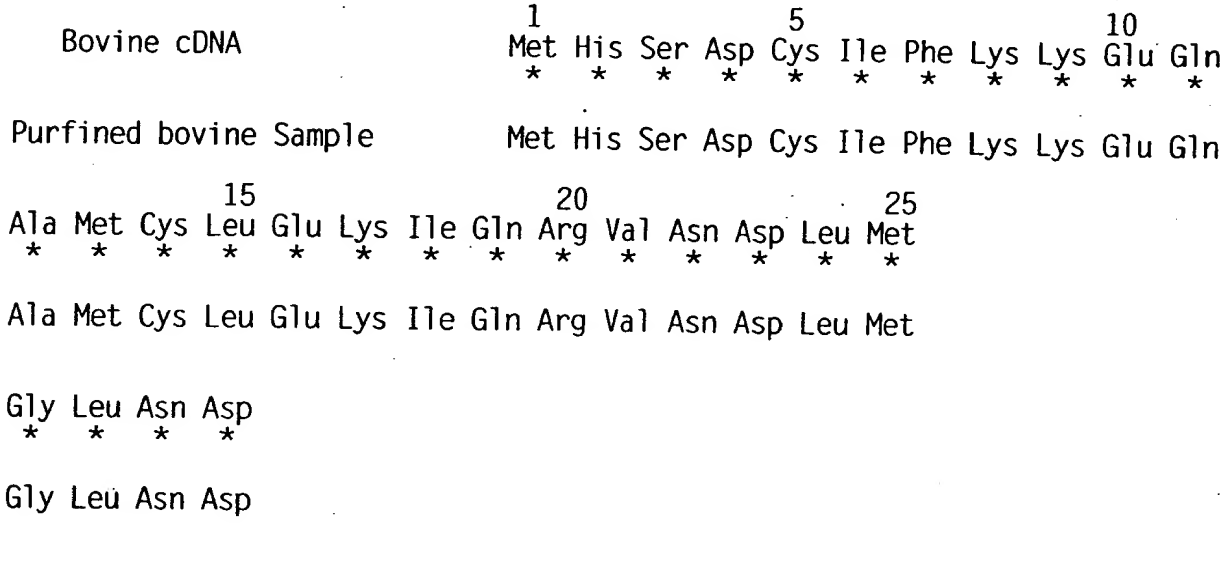


FIG. 4

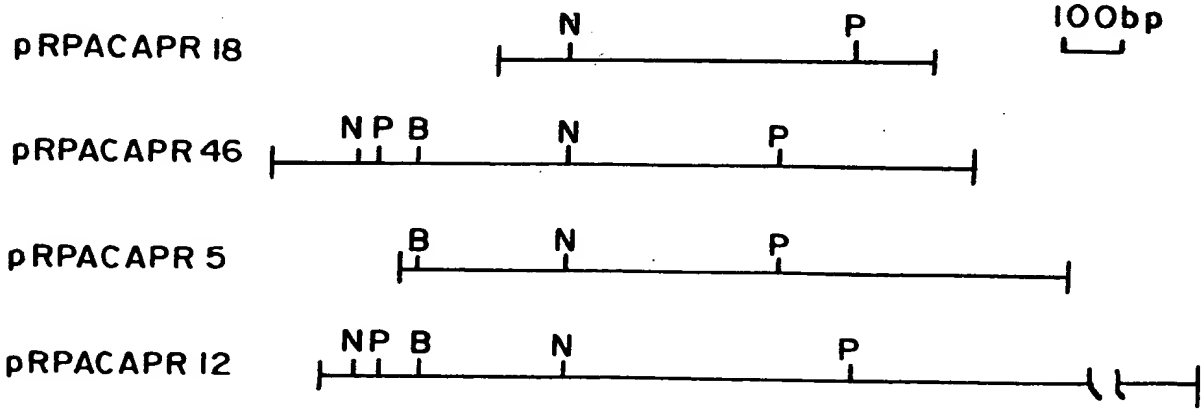


FIG. 6

```
TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTCGCCTCC     60
CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG    120
CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC    180
CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC    240
GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GGCGGACACA    300
CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC    360
GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC    420
CGCAGCCCGC GGCCCCGCCG CGAGGCCCCT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG    480
AGCAGTGGCG GCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT        530
                  Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro
                    1               5                  10

TGC AGG CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT      578
Cys Arg Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala
            15                  20                  25

GCT CTC CTC CTG CTG CCT ATG GCC ACC GCC ATG CAT TCC GAC TGC ATC      626
Ala Leu Leu Leu Leu Pro Met Ala Thr Ala Met His Ser Asp Cys Ile
        30                  35                  40

TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT      674
Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn
    45                  50                  55

GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG      722
Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp
60                  65                  70                  75

GAC AAC ATC ACG TGT TGG AAG CCC GCC CAC GTG GGT GAG ATG GTC CTG      770
Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu
                80                  85                  90

GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG      818
Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp
            95                  100                 105

GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG      866
Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu
        110                 115                 120

GAT CTC TCA GAC ATG AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA      914
Asp Leu Ser Asp Met Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly
    125                 130                 135

TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT GGG TTT GAG GAG      962
Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Glu Glu
140                 145                 150                 155

TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG     1010
Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys
                160                 165                 170
```

FIG. 2A

```
GCC CTG TAC ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT    1058
Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr
            175                 180                 185

GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG CTG CAC TGC ACC CGC AAC    1106
Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn
        190                 195                 200

TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC    1154
Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser
    205                 210                 215

GTC TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC    1202
Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His
220                 225                 230                 235

TGC TTT GTC TCC ACT GTG GAA TGC AAG GCT GTG ATG GTT TTC TTC CAC    1250
Cys Phe Val Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His
                240                 245                 250

TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG TAT    1298
Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr
            255                 260                 265

CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC    1346
Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe
        270                 275                 280

TAC TGG TAC ATC ATC ATT GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT    1394
Tyr Trp Tyr Ile Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Ser
    285                 290                 295

GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC TGC TGG GAT    1442
Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp
300                 305                 310                 315

ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT    1490
Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val
                320                 325                 330

GGC TCC ATA ATG GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC    1538
Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile
            335                 340                 345

CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAC GAG TCC AGC    1586
Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser
        350                 355                 360

ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG CCA CAG CGG GCT    1634
Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala
    365                 370                 375

CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTA CGG    1682
Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg
```

FIG. 2B

```
380                 385                 390                 395

CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT GGA ATC CAC TAC    1730
Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr
                400                 405                 410

ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG AGG GAG AGA CTG    1778
Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu
            415                 420                 425

GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT    1826
Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val
        430                 435                 440

CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG ATC AAG AGG AAG    1874
Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys
    445                 450                 455

TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG GAC TTC AAG CAC    1922
Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His
460                 465                 470                 475

CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC    1970
Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu
                480                 485                 490

TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC CGC ATG TCT GGG CTT CCG    2018
Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro
            495                 500                 505

GCC GAC AAC CTG GCC ACC TGAGCCCACC CTGCCCCCTC CTCTCCTCTG TACGCAGGC  2075
Ala Asp Asn Leu Ala Thr
        510

TGGGGCTGTG GTGGGGCGCC GGCCCACGCA TGTTGTGCCT CTTCTCGCCT TCGGGCAGGC   2135
CCCGGGCTGG GCGCCTGGCC CCCGAGGTTG GAGAAGGATG CGGGACAGGC AGCTGTTTAG   2195
CCTTCCTGTT TTGGCGCTGG CCCAACCACC GTGGGTCCCT GGGCCTGCAC CCAGACATGT   2255
AATACTCCTT AATTGGGAAG TCATCCATTC TTTCCCTTTC CCAAGTCCTT GCTTATTAAG   2315
AGGTTCAAGT CACCTACCCA ATTCAGAAGC TTAAGTAACC ACTAACCACC GTGACTGCGT   2375
GGGAGGCCTC CCATGGGCTG AGCTACTGAC TTGGCTTTGG GGGCCTTGGG CTGGGGCCCT   2435
CCTTAAAGCC CCCCCTGAAA TTGTCGGACC TCAAAGTGTG ACTCCTTTGA GTCTACTCGC   2495
CACCCCCGTG GCCCTTTGCA GCCCTGGTCC AGTCACCGAG GTTACTGGAA GTCCAGCTTG   2555
GATGGCCAGA CAGCTTTTTG GCACAGGCAG ACCCATGCTC ACCCAACATT TTAGTGTCCA   2615
GGTGCCCAGG TGCCCAGGTG CCCAGCTCCT GGGCATCAGA CAGTGGGAAA GCTCCAGGGA   2675
TCTACCATTC AGAGACTTCA GTTTGGATGT AGGGCTAAGG CCAGAGAAAA GTTCTGGAGC   2735
TTTTCATTTG GCCCAAGAAA AAACTGCCAA GATCCAGAAA AGTGGATCTG AGTGGAATTT   2795
AGATGCAAAG AGCTTGGAG                                                2814
```

FIG. 2C

```
TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTCGCCTCC    60
CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG   120
CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC   180
CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC   240
GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GGCGGACACA   300
CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC   360
GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC   420
CGCAGCCCGC GGCCCCGCCG CGAGGCCCCT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG   480
AGCAGTGGCG GCTGTGA ATG AGA GGC GGG CGG CAC TGG CCC GAG CCG CCT       530
                  Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro
                   1               5                  10

TGC AGG CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT     578
Cys Arg Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala
            15                  20                  25

GCT CTC CTC CTG CTG CCT ATG GCC ACC GCC ATG CAT TCC GAC TGC ATC     626
Ala Leu Leu Leu Leu Pro Met Ala Thr Ala Met His Ser Asp Cys Ile
        30                  35 △                40

TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTG AAT     674
Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn
    45                  50                  55

GAC CTG ATG GGC TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG     722
Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp
60                  65                  70                  75

GAC AAC ATC ACG TGT TGG AAG CCC GCC CAC GTG GGT GAG ATG GTC CTG     770
Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu Met Val Leu
                80                  85                  90

GTC AGT TGC CCT GAA CTC TTC CGA ATC TTC AAC CCA GAC CAA GTC TGG     818
Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln Val Trp
            95                  100                 105

GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG     866
Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu
        110                 115                 120

GAT CTC TCA GAC ATG AGG GTG GTG AGC CGG AAT TGC ACG GAG GAT GGA     914
Asp Leu Ser Asp Met Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly
    125                 130                 135

TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT GGG TTT GAG GAG     962
Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Glu Glu
140                 145                 150                 155

TAC GAA TCT GAG ACT GGG GAC CAG GAT TAC TAC TAC CTG TCA GTG AAG    1010
```

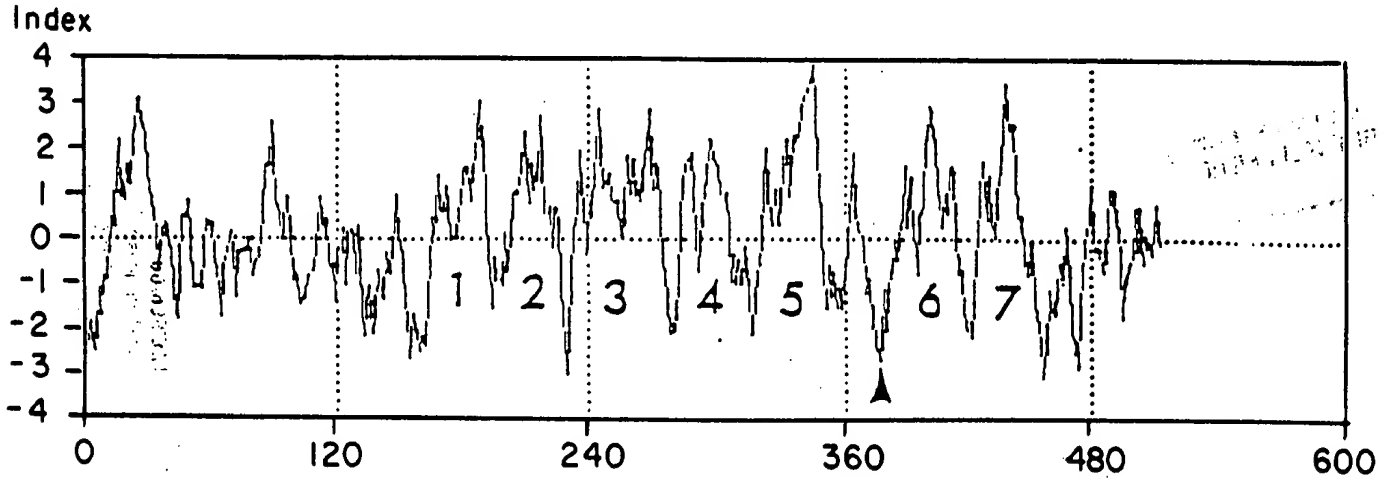
FIG. 3A

```
Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys
                160                 165                 170

GCC CTG TAC ACA GTT GGC TAC AGC ACG TCC CTC GTC ACC CTC ACC ACT    1058
Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr
            175                 180                 185

GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG CTG CAC TGC ACC CGC AAC    1106
Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn
        190                 195                 200

TTC ATC CAC ATG AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC    1154
Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser
    205                 210                 215

GTC TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC    1202
Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His
220                 225                 230                 235

TGC TTT GTC TCC ACT GTG GAA TGC AAG GCT GTG ATG GTT TTC TTC CAC    1250
Cys Phe Val Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His
                240                 245                 250

TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG TAT    1298
Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr
            255                 260                 265

CTC TTC ACC CTG CTG GTG GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC    1346
Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe
        270                 275                 280

TAC TGG TAC ATC ATC ATT GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT    1394
Tyr Trp Tyr Ile Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Ser
    285                 290                 295

GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC TGC TGG GAT    1442
Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp
300                 305                 310                 315

ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT    1490
Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val
                320                 325                 330

GGC TCC ATA ATG GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC    1538
Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile
            335                 340                 345

CTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA GGC AAC GAG TCC AGC    1586
Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser
        350                 355                 360

ATC TAC TTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC CCA CTC TTT    1634
Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe
    365                 370                 375
```

FIG. 3B

```
GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC AGC AAG      1682
Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys
380                 385                 390                 395

AGG GAG AGA CTG GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT      1730
Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe
                400                 405                 410

GTG GTG GCT GTT CTC TAT TGC TTT CTG AAT GGA GAG GTG CAG GCG GAG      1778
Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu
            415                 420                 425

ATC AAG AGG AAG TGG CGG AGC TGG AAG GTG AAC CGC TAC TTC ACC ATG      1826
Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met
        430                 435                 440

GAC TTC AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG      1874
Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly
    445                 450                 455

GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAG ATC CGC ATG      1922
Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met
460                 465                 470                 475

TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGAGCCCACC CTGCCCCCTC CTCT   1976
Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
                480                 485

CCTCTGTACG CAGGCTGGGG CTGTGGTGGG GCGCCGGCCC ACGCATGTTG TGCCTCTTCT   2036
CGCCTTCGGG CAGGCCCCGG GCTGGGCGCC TGGCCCCCGA GGTTGGAGAA GGATGCGGGA   2096
CAGGCAGCTG TTTAGCCTTC CTGTTTTGGC GCTGGCCCAA CCACCGTGGG TCCCTGGGCC   2156
TGCACCCAGA CATGTAATAC TCCTTAATTG GGAAGTCATC CATTCTTTCC CTTTCCCAAG   2216
TCCTTGCTTA TTAAGAGGTT CAAGTCACCT ACCCAATTCA GAAGCTTAAG TAACCACTAA   2276
CCACCGTGAC TGCGTGGGAG GCCTCCCATG GGCTGAGCTA CTGACTTGGC TTTGGGGGCC   2336
TTGGGCTGGG GCCCTCCTTA AAGCCCCCCC TGAAATTGTC GGACCTCAAA GTGTGACTCC   2396
TTTGAGTCTA CTCGCCACCC CCGTGGCCCT TTGCAGCCCT GGTCCAGTCA CCGAGGTTAC   2456
TGGAAGTCCA GCTTGGATGG CCAGACAGCT TTTTGGCACA GGCAGACCCA TGCTCACCCA   2516
ACATTTTAGT GTCCAGGTGC CCAGGTGCCC AGGTGCCCAG CTCCTGGGCA TCAGACAGTG   2576
GGAAAGCTCC AGGGATCTAC CATTCAGAGA CTTCAGTTTG GATGTAGGGC TAAGGCCAGA   2636
GAAAAGTTCT GGAGCTTTTC ATTTGGCCCA AGAAAAAACT GCCAAGATCC AGAAAAGTGG   2696
ATCTGAGTGG AATTTAGATG CAAAGAGCTT GGAG                               2730
```

FIG. 3C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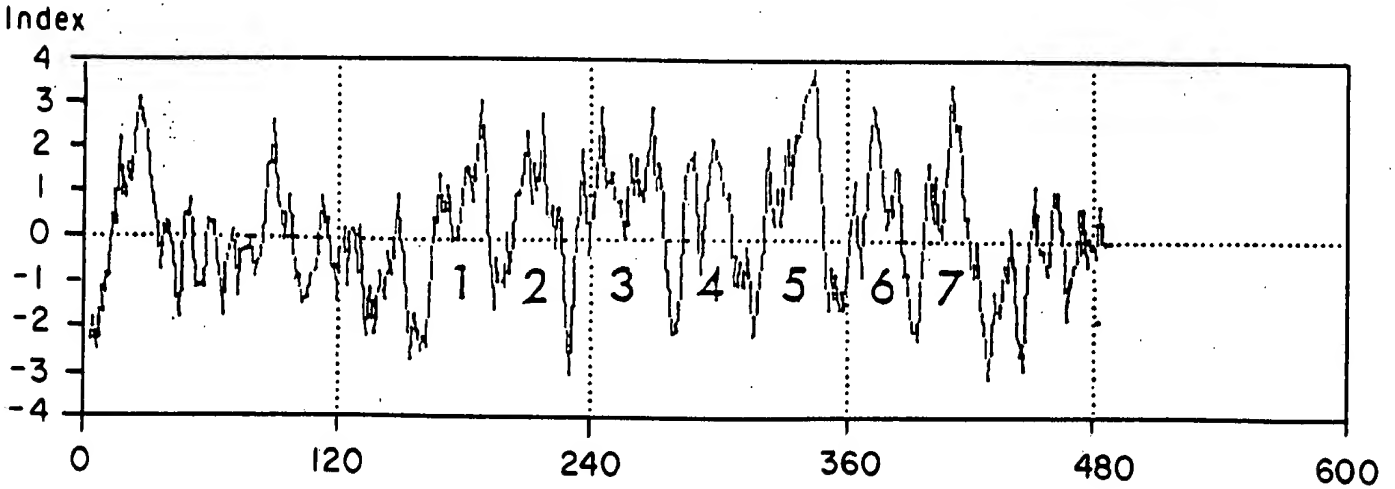
1
0
-1
-2
-3
-4
1
2
3
4
5
6
7
0
120
240
360
480
600

FIG. 5A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1
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-1
-2
-3
-4
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2
3
4
5
6
7
0
120
240
360
480
600

FIG. 5B

```
CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA      60
GTGGCTGGGA AGCACC ATG GCC AGA GTC CTG CAG CTC TCC CTG ACT GCT CTC     112
                  Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu
                   1               5                  10

CTG CTG CCT GTG GCT ATT GCT ATG CAC TCT GAC TGC ATC TTC AAG AAG      160
Leu Leu Pro Val Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys
        15                  20                  25

GAG CAA GCC ATG TGC CTG GAG AGG ATC CAG AGG GCC AAC GAC CTG ATG      208
Glu Gln Ala Met Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met
    30                  35                  40

GGA CTA AAC GAG TCT TCC CCA GGT TGC CCT GGC ATG TGG GAC AAT ATC      256
Gly Leu Asn Glu Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile
45                  50                  55                  60

ACA TGT TGG AAG CCA GCT CAA GTA GGT GAG ATG GTC CTT GTA AGC TGC      304
Thr Cys Trp Lys Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys
                65                  70                  75

CCT GAG GTC TTC CGG ATC TTC AAC CCG GAC CAA GTC TGG ATG ACA GAA      352
Pro Glu Val Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu
            80                  85                  90

ACC ATA GGA GAT TCT GGT TTT GCC GAT AGT AAT TCC TTG GAG ATC ACA      400
Thr Ile Gly Asp Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr
        95                  100                 105

GAC ATG GGG GTC GTG GGC CGG AAC TGC ACA GAG GAC GGC TGG TCG GAG      448
Asp Met Gly Val Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu
    110                 115                 120

CCC TTC CCC CAC TAC TTC GAT GCT TGT GGG TTT GAT GAT TAT GAG CCT      496
Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro
125                 130                 135                 140

GAG TCT GGA GAT CAG GAT TAT TAC TAC CTG TCG GTG AAG GCT CTC TAC      544
Glu Ser Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr
                145                 150                 155

ACA GTC GGC TAC AGC ACT TCC CTC GCC ACC CTC ACT ACT GCC ATG GTC      592
Thr Val Gly Tyr Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val
            160                 165                 170

ATC TTG TGC CGC TTC CGG AAG CTG CAT TGC ACT CGC AAC TTC ATC CAC      640
Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His
        175                 180                 185

ATG AAC CTG TTT GTA TCC TTC ATG CTG AGG GCT ATC TCC GTC TTC ATC      688
Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile
```

FIG. 7A

```
    190                 195                 200

AAG GAC TGG ATC TTG TAC GCC GAG CAG GAC AGC AGT CAC TGC TTC GTT   736
Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Ser His Cys Phe Val
205                 210                 215                 220

TCC ACC GTG GAG TGC AAA GCT GTC ATG GTT TTC TTC CAC TAC TGC GTG   784
Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val
                225                 230                 235

GTG TCC AAC TAC TTC TGG CTG TTC ATT GAA GGC CTG TAC CTC TTT ACA   832
Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr
            240                 245                 250

CTG CTG GTG GAG ACC TTC TTC CCT GAG AGG AGA TAT TTC TAC TGG TAC   880
Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr
        255                 260                 265

ACC ATC ATC GGC TGG GGG ACA CCT ACT GTG TGT GTA ACA GTG TGG GCT   928
Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala
    270                 275                 280

GTG CTG AGG CTC TAT TTT GAT GAT GCA GGA TGC TGG GAT ATG AAT GAC   976
Val Leu Arg Leu Tyr Phe Asp Asp Ala Gly Cys Trp Asp Met Asn Asp
285                 290                 295                 300

AGC ACA GCT CTG TGG TGG GTG ATC AAA GGC CCC GTG GTT GGC TCT ATA  1024
Ser Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile
                305                 310                 315

ATG GTT AAC TTT GTG CTT TTC ATC GGC ATC ATC ATC ATC CTT GTA CAG  1072
Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Ile Ile Leu Val Gln
            320                 325                 330

AAG CTG CAG TCC CCA GAC ATG GGA GGC AAC GAG TCC AGC ATC TAC TTA  1120
Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu
        335                 340                 345

CGG CTG GCC CGC TCC ACC CTA CTG CTC ATC CCA CTC TTC GGA ATC CAC  1168
Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His
    350                 355                 360

TAC ACA GTA TTC GCC TTC TCT CCA GAG AAC GTC AGC AAG AGG GAA AGA  1216
Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg
365                 370                 375                 380

CTT GTG TTT GAG CTT GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT  1264
Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala
                385                 390                 395

GTA CTC TAC TGC TTC CTG AAT GGG GAG GTA CAG GCA GAG ATT AAG AGG  1312
Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg
            400                 405                 410
```

FIG. 7B

```
AAA TGG AGG AGC TGG AAG GTG AAC CGT TAC TTC ACT ATG GAC TTC AAG    1360
Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys
        415                 420                 425

CAC CGG CAC CCG TCC CTG GCC AGC AGT GGA GTA AAT GGG GGA ACC CAG    1408
His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln
    430                 435                 440

CTG TCC ATC CTG AGC AAG AGC AGC TCC CAG CTC CGC ATG TCC AGC CTC    1456
Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu
445                 450                 455                 460

CCG GCC GAC AAC TTG GCC ACC TGAGGCCTGT CTCCCTCCTC CTTCTGCACA GGCTG  1512
Pro Ala Asp Asn Leu Ala Thr ***
                465

GGGCTGCGGG CCAGTGCCTG AGCATGTTTG TGCCTCTCCC CTCTCCTTGG GCAGGCCCTG   1572
GGTAGGAAGC TGGGCTCCTC CCCAAAGGGG AAGAGAGAGA TAGGGTATAG GCTGATATTG   1632
CTCCTCCTGT TTGGGTCCCA CCTACTGTGA TTCATTGAGC CTGATTTGAC ATGTAAATAC   1692
ACCTCAAATT TGGAAAGTTG CCCCATCTCT GCCCCCAACC CATGCCCCTG CTCACCTCTG   1752
CCAGGCCCCA GCTCAACCTA CTGTGTCAAG GCCAGCCTCA GTGATAGTCT GATCCCAGGT   1812
ACAAGGCCTT GTGAGCTGAG GCTGAAAGGC CTGTTTTGGA GAGGCTGGGG TAGTGCC      1869
```

FIG. 8

```
CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA    60
GTGGCTGGGA AGCACC ATG GCC AGA GTC CTG CAG CTC TCC CTG ACT GCT CTC   112
                  Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu
                   1               5                  10

CTG CTG CCT GTG GCT ATT GCT ATG CAC TCT GAC TGC ATC TTC AAG AAG     160
Leu Leu Pro Val Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys
        15                  △20                 25

GAG CAA GCC ATG TGC CTG GAG AGG ATC CAG AGG GCC AAC GAC CTG ATG     208
Glu Gln Ala Met Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met
    30                  35                  40

GGA CTA AAC GAG TCT TCC CCA GGT TGC CCT GGC ATG TGG GAC AAT ATC     256
Gly Leu Asn Glu Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile
45                  50                  55                  60

ACA TGT TGG AAG CCA GCT CAA GTA GGT GAG ATG GTC CTT GTA AGC TGC     304
Thr Cys Trp Lys Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys
                65                  70                  75

CCT GAG GTC TTC CGG ATC TTC AAC CCG GAC CAA GTC TGG ATG ACA GAA     352
Pro Glu Val Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu
            80                  85                  90

ACC ATA GGA GAT TCT GGT TTT GCC GAT AGT AAT TCC TTG GAG ATC ACA     400
Thr Ile Gly Asp Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr
        95                  100                 105

GAC ATG GGG GTC GTG GGC CGG AAC TGC ACA GAG GAC GGC TGG TCG GAG     448
Asp Met Gly Val Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu
    110                 115                 120

CCC TTC CCC CAC TAC TTC GAT GCT TGT GGG TTT GAT GAT TAT GAG CCT     496
Pro Phe Pro His Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro
125                 130                 135                 140

GAG TCT GGA GAT CAG GAT TAT TAC TAC CTG TCG GTG AAG GCT CTC TAC     544
Glu Ser Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr
                145                 150                 155

ACA GTC GGC TAC AGC ACT TCC CTC GCC ACC CTC ACT ACT GCC ATG GTC     592
Thr Val Gly Tyr Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val
            160                 165                 170

ATC TTG TGC CGC TTC CGG AAG CTG CAT TGC ACT CGC AAC TTC ATC CAC     640
Ile Leu Cys Arg Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His
        175                 180                 185

ATG AAC CTG TTT GTA TCC TTC ATG CTG AGG GCT ATC TCC GTC TTC ATC     688
Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile
    190                 195                 200
```

FIG. 9A

```
AAG GAC TGG ATC TTG TAC GCC GAG CAG GAC AGC AGT CAC TGC TTC GTT      736
Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Ser His Cys Phe Val
205                 210                 215                 220

TCC ACC GTG GAG TGC AAA GCT GTC ATG GTT TTC TTC CAC TAC TGC GTG      784
Ser Thr Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val
                225                 230                 235

GTG TCC AAC TAC TTC TGG CTG TTC ATT GAA GGC CTG TAC CTC TTT ACA      832
Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr
            240                 245                 250

CTG CTG GTG GAG ACC TTC TTC CCT GAG AGG AGA TAT TTC TAC TGG TAC      880
Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr
        255                 260                 265

ACC ATC ATC GGC TGG GGG ACA CCT ACT GTG TGT GTA ACA GTG TGG GCT      928
Thr Ile Ile Gly Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala
    270                 275                 280

GTG CTG AGG CTC TAT TTT GAT GAT GCA GGA TGC TGG GAT ATG AAT GAC      976
Val Leu Arg Leu Tyr Phe Asp Asp Ala Gly Cys Trp Asp Met Asn Asp
285                 290                 295                 300

AGC ACA GCT CTG TGG TGG GTG ATC AAA GGC CCC GTG GTT GGC TCT ATA     1024
Ser Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile
                305                 310                 315

ATG GTT AAC TTT GTG CTT TTC ATC GGC ATC ATC ATC ATC CTT GTA CAG     1072
Met Val Asn Phe Val Leu Phe Ile Gly Ile Ile Ile Ile Leu Val Gln
            320                 325                 330

AAG CTG CAG TCC CCA GAC ATG GGA GGC AAC GAG TCC AGC ATC TAC TTC     1120
Lys Leu Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe
        335                 340                 345                 Δ

AGC TGC GTG CAG AAA TGC TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC     1168
Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala Gln Gln His
    350                 355                 360

TCT TGC AAG ATG TCA GAA CTA TCC ACC ATT ACT CTA CGG CTG GCC CGC     1216
Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg
365                 370                 375                 Δ   380

TCC ACC CTA CTG CTC ATC CCA CTC TTC GGA ATC CAC TAC ACA GTA TTC     1264
Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe
                385                 390                 395

GCC TTC TCT CCA GAG AAC GTC AGC AAG AGG GAA AGA CTT GTG TTT GAG     1312
Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu
            400                 405                 410

CTT GGG CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTA CTC TAC TGC     1360
Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys
```

FIG. 9B

```
          415                 420                 425

TTC CTG AAT GGG GAG GTA CAG GCA GAG ATT AAG AGG AAA TGG AGG AGC    1408
Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser
    430                 435                 440

TGG AAG GTG AAC CGT TAC TTC ACT ATG GAC TTC AAG CAC CGG CAC CCG    1456
Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro
445                 450                 455                 460

TCC CTG GCC AGC AGT GGA GTA AAT GGG GGA ACC CAG CTG TCC ATC CTG    1504
Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu
                465                 470                 475

AGC AAG AGC AGC TCC CAG CTC CGC ATG TCC AGC CTC CCG GCC GAC AAC    1552
Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn
            480                 485                 490

TTG GCC ACC TGAGGCCTGT CTCCCTCCTC CTTCTGCACA GGCTGGGGCT GCGGGCCAGT 1611
Leu Ala Thr
        495

GCCTGAGCAT GTTTGTGCCT CTCCCCTCTC CTTGGGCAGG CCCTGGGTAG GAAGCTGGGC   1671
TCCTCCCCAA AGGGGAAGAG AGAGATAGGG TATAGGCTGA TATTGCTCCT CCTGTTTGGG   1731
TCCCACCTAC TGTGATTCAT TGAGCCTGAT TTGACATGTA AATACACCTC AAATTTGGAA   1791
AGTTGCCCCA TCTCTGCCCC CAACCCATGC CCCTGCTCAC CTCTGCCAGG CCCCAGCTCA   1851
ACCTACTGTG TCAAGGCCAG CCTCAGTGAT AGTCTGATCC CAGGTACAAG GCCTTGTGAG   1911
CTGAGGCTGA AAGGCCTGTT TTGGAGAGGC TGGGGTAGTG CCCACCCCAG CAGCCTTTCA   1971
GCAAATTGAC TTTGGATGTG GACCCTTCTC AGCCTGTACC AAGTACTGCA GTTGGCTAGG   2031
GATGCAGCTC AGTTTCCTGA GCATCCTTTG GAGCAGGTCA ACCTGAGGCT CCTTTTGCTT   2091
ACCCGACATC TAAGTTGTCC AGGTGCTCGG CTCCTGTGTG CCTGGATGAC GGGAGGGCTC   2151
CGGGGTCTTT CAGTCAAAGA CTTACATTGA GGTGGGGTGA GAGTCAGAGA AAAGTTCTGG   2211
TGCTTTTCAT TTGTTCTAAG AGCTGAGAGC CAGGAATGCA GAGTCAATTG GGAAGGAGAT   2271
GGGATAGCTG ATGATCTTAC CATGTCCATG ACTGTGCCCC TGATTCAAGA CCGGATCATG   2331
TGGTGGCTTT ATTTCTACAC TTCTTGTCCA CAATGGACAG TCTGAGGAAG CTCTTCTTTC   2391
AGCCACAACA ACCACAGAAA GCCCTTTCTT CTCCCCTCTT GTTTCTCCAT AAGTCAAAGC   2451
CATGTTTAGA ACGGACCAGC CACCTTGCGA TGAAATCACT GAGTTCTGAA GCAACTTTCA   2511
ATTTCCACGA GCCAAGTCCT GGGTCCAGGG ACGCCCC                            2548
```

FIG. 10

Rat	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	1				5					10					15	

Rat	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu
	*	*	*		*	*	*	*	*	*	*	*	
Bovine	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp
				20					25				

FIG. 11

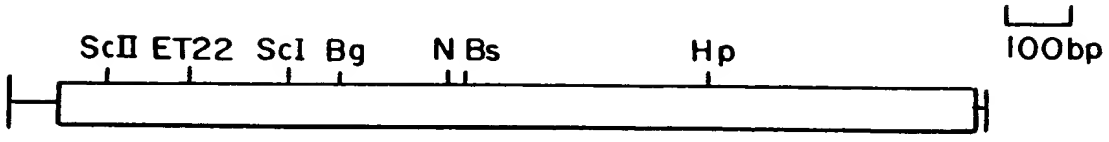


FIG. 12

					5					10						15
Human	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	

					20					25						
Human	Gly	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp		
	*	*	*	*	*	*	*	*	*	*	*	*	*	*		
Bovine	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp		

FIG. 14

```
AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG    60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC      109
               Met Ala Gly Val Val His Val Ser Leu Ala Ala His
               1               5                   10

TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA     157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala
        15                  20                  25

GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG     205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu
    30                  35                  40

CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT     253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly
45                  50                  55                  60

GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT     301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro
                65                  70                  75

GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG     349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu
            80                  85                  90

GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT     397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser
        95                  100                 105

CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC     445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala
    110                 115                 120

CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC     493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile
125                 130                 135                 140

TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT     541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp
                145                 150                 155

TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC     589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser
            160                 165                 170

CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT     637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe
        175                 180                 185

GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT     685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp
```

FIG. 13A

```
    190                 195                 200

TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA      733
Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr
205                 210                 215                 220

TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG      781
Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg
                225                 230                 235

AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG      829
Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser
            240                 245                 250

TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT      877
Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr
        255                 260                 265

GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG      925
Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys
    270                 275                 280

GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG      973
Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp
285                 290                 295                 300

CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC     1021
Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe
                305                 310                 315

TTC CCT GAA AGG AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG     1069
Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly
            320                 325                 330

TCC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG CTG AGA CTC TAC TTT     1117
Ser Pro Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe
        335                 340                 345

GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG     1165
Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp
    350                 355                 360

GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT     1213
Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu
365                 370                 375                 380

TTT ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC     1261
Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp
                385                 390                 395

ATG GGA GGC AAT GAG TCC AGC ATC TAC TTG CGA CTG GCC CGG TCC ACC     1309
Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr
            400                 405                 410
```

FIG. 13B

```
CTG CTG CTC ATC CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC      1357
Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe
        415                 420                 425

TCC CCA GAG AAT GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG      1405
Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly
    430                 435                 440

CTG GGC TCC TTC CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG      1453
Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu
445                 450                 455                 460

AAT GGT GAG GTA CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG      1501
Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys
                465                 470                 475

GTG AAC CGT TAC TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG      1549
Val Asn Arg Tyr Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu
            480                 485                 490

GCC AGC AGT GGG GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG      1597
Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys
        495                 500                 505

AGC AGC TCC CAA ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC      1645
Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala
    510                 515                 520

ACC TGAGCCATGC TCCCCT                                               1664
Thr
525
```

FIG. 13C

```
Rat             Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
Type I-B        AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAA

pHRP15A         Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys
human Type I-B  AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG

pHPR55A         Asn Glu Ser Ser Ile Tyr Phe ___ Cys Val Gln Lys Cys Tyr Cys Lys
Type I-B2       AAT GAG TCC AGC ATC TAC TTC     TGC GTG CAG AAA TGC TAC TGC AAG

pHRP66P         Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg Val Pro Lys
Type I-C        AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA GTC CCC AAG

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG CGT CAG CAG CAC TCT TGC AAG ATC TCA GAA CTA TCC ACC

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC

Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr
CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC

Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln His Ser Leu
AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG CAT TCA CTC

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTA CGG CTG GCC CGC TCC ACC CTA

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG

Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu
ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG

Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu
CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG
```

FIG. 15

```
AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG      60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC          109
               Met Ala Gly Val Val His Val Ser Leu Ala Ala His
                1               5                  10

TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA         157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala
        15                  20                  25

GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG         205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu
    30                  35                  40

CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT         253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly
45                  50                  55                  60

GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT         301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro
                65                  70                  75

GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG         349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu
            80                  85                  90

GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT         397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser
        95                  100                 105

CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC         445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala
    110                 115                 120

CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC         493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile
125                 130                 135                 140

TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT         541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp
                145                 150                 155

TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC         589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser
            160                 165                 170

CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT         637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe
        175                 180                 185

GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT         685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp
```

FIG. 16A

```
    190                 195                 200

TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA      733
Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr
205                 210                 215                 220

TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG      781
Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg
                225                 230                 235

AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG      829
Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser
            240                 245                 250

TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT      877
Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr
        255                 260                 265

GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG      925
Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys
    270                 275                 280

GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG      973
Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp
285                 290                 295                 300

CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC     1021
Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe
                305                 310                 315

TTC CCT GAA AGG AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG     1069
Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly
            320                 325                 330

ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG CTG AGA CTC TAC TTT     1117
Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe
        335                 340                 345

GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG     1165
Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp
    350                 355                 360

GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT     1213
Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu
365                 370                 375                 380

TTT ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC     1261
Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp
                385                 390                 395

ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC     1309
Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys
            400                 405                 410
```

FIG. 16B

```
TAC TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA      1357
Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu
        415                 420                 425

CTG TCC ACC ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC      1405
Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile
    430                 435                 440

CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT      1453
Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn
445                 450                 455                 460

GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC      1501
Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe
                465                 470                 475

CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA      1549
Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val
            480                 485                 490

CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC      1597
Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr
        495                 500                 505

TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG      1645
Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly
    510                 515                 520

GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA      1693
Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln
525                 530                 535                 540

ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCC   1745
Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
                545                 550

CCT                                                                  1748
```

FIG. 16C

```
AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG      60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC          109
               Met Ala Gly Val Val His Val Ser Leu Ala Ala His
                1               5                  10

TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA         157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala
        15                  20                  25

GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG         205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu
    30                  35                  40

CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT         253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly
45                  50                  55                  60

GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT         301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro
                65                  70                  75

GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG         349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu
            80                  85                  90

GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT         397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser
        95                  100                 105

CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC         445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala
    110                 115                 120

CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC         493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile
125                 130                 135                 140

TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT         541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp
                145                 150                 155

TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC         589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser
            160                 165                 170

CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT         637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe
        175                 180                 185

GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT         685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp
    190                 195                 200
```

FIG. 17A

```
TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA      733
Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr
205                 210                 215                 220

TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG      781
Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg
                225                 230                 235

AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG      829
Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser
            240                 245                 250

TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT      877
Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr
        255                 260                 265

GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG      925
Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys
    270                 275                 280

GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG      973
Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp
285                 290                 295                 300

CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC     1021
Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe
                305                 310                 315

TTC CCT GAA AGG AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG     1069
Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly
            320                 325                 330

ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG CTG AGA CTC TAC TTT     1117
Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe
        335                 340                 345

GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG     1165
Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp
    350                 355                 360

GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT     1213
Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu
365                 370                 375                 380

TTT ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC     1261
Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp
                385                 390                 395

ATG GGA GGC AAT GAG TCC AGC ATC TAC TTC TGC GTG CAG AAA TGC TAC     1309
Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr
            400                 405                 410

TGC AAG CCA CAG CGG GCT CAG CAG CAC TCT TGC AAG ATG TCA GAA CTG     1357
Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu
```

FIG. 17B

```
                415                 420                 425

TCC ACC ATT ACT CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC CCA    1405
Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro
    430                 435                 440

CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT GTC    1453
Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val
445                 450                 455                 460

AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC CAG    1501
Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln
                465                 470                 475

GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA CAA    1549
Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln
            480                 485                 490

GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC TTC    1597
Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe
        495                 500                 505

GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG GTG    1645
Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val
    510                 515                 520

AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA ATC    1693
Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile
525                 530                 535                 540

CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCCCCT   1745
Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
                545                 550
```

FIG. 17C

```
AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG      60
GCCAAGAAGT GTC ATG GCT GGT GTC GTG CAC GTT TCC CTG GCT GCT CAC          109
               Met Ala Gly Val Val His Val Ser Leu Ala Ala His
                1               5                  10

TGC GGG GCC TGT CCG TGG GGC CGG GGC AGA CTC CGC AAA GGA CGC GCA         157
Cys Gly Ala Cys Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala
        15                  20                  25

GCC TGC AAG TCC GCG GCC CAG AGA CAC ATT GGG GCT GAC CTG CCG CTG         205
Ala Cys Lys Ser Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu
    30                  35                  40

CTG TCA GTG GGA GGC CAG TGG TGC TGG CCA AGA AGT GTC ATG GCT GGT         253
Leu Ser Val Gly Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly
45                  50                  55                  60

GTC GTG CAC GTT TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC CCT         301
Val Val His Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro
                65                  70                  75

GCC ATG CAT TCT GAC TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG         349
Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu
            80                  85                  90

GAG AAG ATC CAG AGG GCC AAT GAG CTG ATG GGC TTC AAT GAT TCC TCT         397
Glu Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser
        95                  100                 105

CCA GGC TGT CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG CCC GCC         445
Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala
    110                 115                 120

CAT GTG GGT GAG ATG GTC CTG GTC AGC TGC CCT GAG CTC TTC CGA ATC         493
His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile
125                 130                 135                 140

TTC AAC CCA GAC CAA GTC TGG GAG ACC GAA ACC ATT GGA GAG TCT GAT         541
Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp
                145                 150                 155

TTT GGT GAC AGT AAC TCC TTA GAT CTC TCA GAC ATG GGA GTG GTG AGC         589
Phe Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser
            160                 165                 170

CGG AAC TGC ACG GAG GAT GGC TGG TCG GAA CCC TTC CCT CAT TAC TTT         637
Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe
        175                 180                 185

GAT GCC TGT GGG TTT GAT GAA TAT GAA TCT GAG ACT GGG GAC CAG GAT         685
Asp Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp
```

FIG. 18A

```
                190                 195                 200

TAT TAC TAC CTG TCA GTG AAG GCC CTC TAC ACG GTT GGC TAC AGC ACA      733
Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr
205                 210                 215                 220

TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTT TGT CGC TTC CGG      781
Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg
                225                 230                 235

AAG CTG CAC TGC ACA CGC AAC TTC ATC CAC ATG AAC CTG TTT GTG TCG      829
Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser
            240                 245                 250

TTC ATG CTG AGG GCG ATC TCC GTC TTC ATC AAA GAC TGG ATT CTG TAT      877
Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr
        255                 260                 265

GCG GAG CAG GAC AGC AAC CAC TGC TTC ATC TCC ACT GTG GAA TGT AAG      925
Ala Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys
    270                 275                 280

GCC GTC ATG GTT TTC TTC CAC TAC TGT GTT GTG TCC AAC TAC TTC TGG      973
Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp
285                 290                 295                 300

CTG TTC ATC GAG GGC CTG TAC CTC TTC ACT CTG CTG GTG GAG ACC TTC     1021
Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe
                305                 310                 315

TTC CCT GAA AGG AGA TAC TTC TAC TGG TAC ACC ATC ATT GGC TGG GGG     1069
Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly
            320                 325                 330

ACC CCA ACT GTG TGT GTG ACA GTG TGG GCT ACG CTG AGA CTC TAC TTT     1117
Thr Pro Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe
        335                 340                 345

GAT GAC ACA GGC TGC TGG GAT ATG AAT GAC AGC ACA GCT CTG TGG TGG     1165
Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp
    350                 355                 360

GTG ATC AAA GGC CCT GTG GTT GGC TCT ATC ATG GTT AAC TTT GTG CTT     1213
Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu
365                 370                 375                 380

TTT ATT GGC ATT ATC GTC ATC CTT GTG CAG AAA CTT CAG TCT CCA GAC     1261
Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp
                385                 390                 395

ATG GGA GGC AAT GAG TCC AGC ATC TAC TTA ACA AAT TTA AGC CCG CGA     1309
Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Thr Asn Leu Ser Pro Arg
            400                 405                 410
```

FIG. 18B

```
GTC CCC AAG AAA GCC CGA GAG GAC CCC CTG CCT GTG CCC TCA GAC CAG      1357
Val Pro Lys Lys Ala Arg Glu Asp Pro Leu Pro Val Pro Ser Asp Gln
        415                 420                 425

CAT TCA CTC CCT TTC CTG CGA CTG GCC CGG TCC ACC CTG CTG CTC ATC      1405
His Ser Leu Pro Phe Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile
    430                 435                 440

CCA CTA TTC GGA ATC CAC TAC ACA GTA TTT GCC TTC TCC CCA GAG AAT      1453
Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn
445                 450                 455                 460

GTC AGC AAA AGG GAA AGA CTC GTG TTT GAG CTG GGG CTG GGC TCC TTC      1501
Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe
                465                 470                 475

CAG GGC TTT GTG GTG GCT GTT CTC TAC TGT TTT CTG AAT GGT GAG GTA      1549
Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val
            480                 485                 490

CAA GCG GAG ATC AAG CGA AAA TGG CGA AGC TGG AAG GTG AAC CGT TAC      1597
Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr
        495                 500                 505

TTC GCT GTG GAC TTC AAG CAC CGA CAC CCG TCT CTG GCC AGC AGT GGG      1645
Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly
    510                 515                 520

GTG AAT GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG AGC AGC TCC CAA      1693
Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln
525                 530                 535                 540

ATC CGC ATG TCT GGC CTC CCT GCT GAC AAT CTG GCC ACC TGAGCCATGC TCC   1745
Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr ***
                545                 550

CCT                                                                  1748
```

FIG. 18C

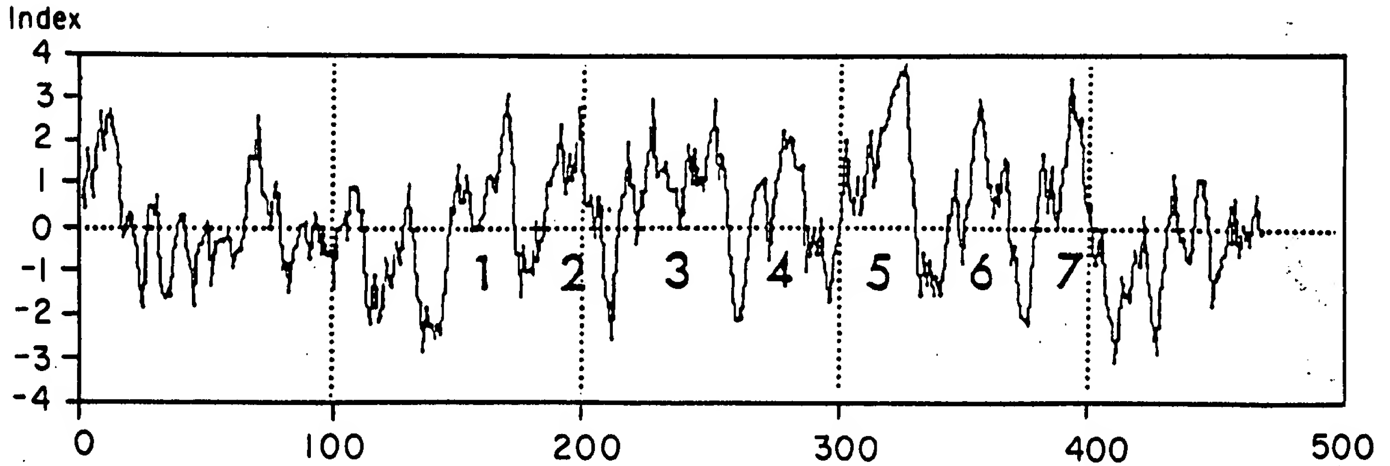


FIG. 19A

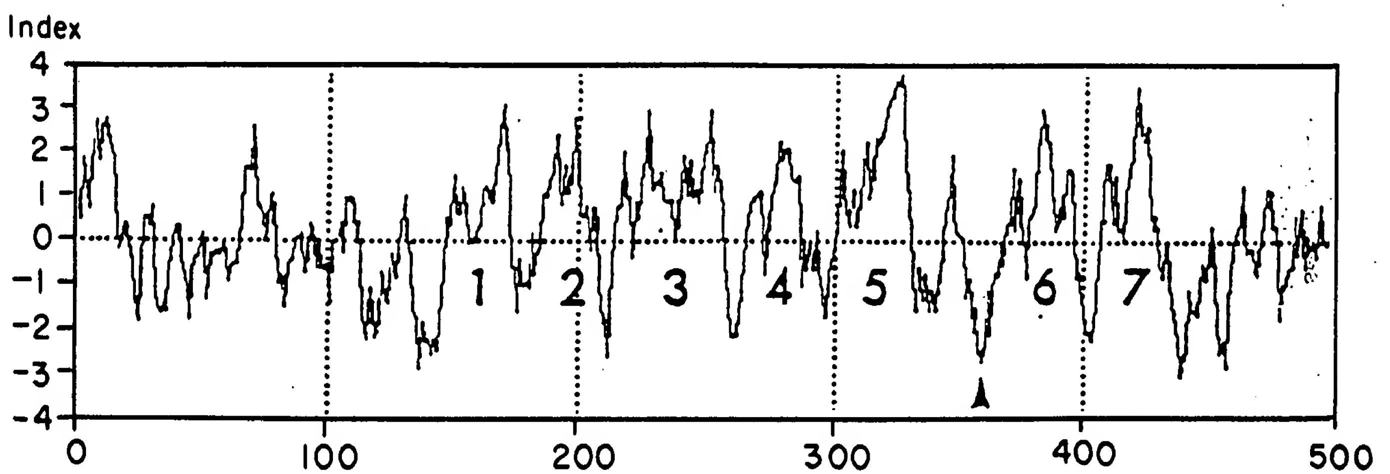


FIG. 19B

```
        19         29         39         49         59         69         79
TALLLPVAIAMHSDCIFKKEQAMCLERIQRANDLMGLNESSPGCPGMWDNITCWKPAQVGEMVLVSCPEV
     * *              **      * *       *          * *       * *         **
MRPPSPPHVRWLCVLAGALACALRPAGSQAASPQHECEYLQLIEIQRQQCLEEAQLENETTGCSKMWDNL
        10         20         30         40         50         60         70

        89         99        109        119        129        139        149
FRIFNPDQVWMTETIGDSGFADSNSLEITDMGVVGRNCTEDGWSEPFPHYFDACGFDDYEPESGDQDYYY
     *              *    **   ***    * *      * *  *   *        * *** **
TCWPTTPRGQAVVLDCPLIFQLFAPIHGYNISRSCTEEGWSQLEPGPYHIACGLNDRASSLDEQQQTKFY
        80         90        100        110        120        130        140

       159        169        179        189        199        209        219
LSVKALYTVGYSTSLATLTTAMVILCRFRKLHCTRNFIHMNLFVSFMLRAISVFIKDWILYAEQDSSHCF
 **** ****** *****  ** **  ********** ********* ******  **   *  **
NTVKTGYTIGYSLSLASLLVAMAILSLFRKLHCTRNYIHMHLFMSFILRATAVFIKDMALFNSGEIDHCS
       150        160        170        180        190        200        210

       229        239        249        259        269        279        289
VSTVECKAVMVFFHYCVVSNYFWLFIEGLYLFTLLVETFFPERRYFYWYTIIGWGTPTVCVTVWAVLRLY
 *** *** **** ********** **********  ********** * ***** *** **********
EASVGCKAAVVFFQYCVMANFFWLLVEGLYLYTLLAVSFFSERKYFWGYILIGWGVPSVFITIWTVVRIY
       220        230        240        250        260        270        280

       299        309        319        329        339        349        359
FDDAGCWDMNDSTALWWVIKGPVVGSIMVNFVLFIGIIIILVQKLQSPDMGGNESSIYLRLARSTLLLIP
*** ****    ********** ********** ** ****** ***** **** * **********
FEDFGCWDTIINSSLWWIIKAPILLSILVNFVLFICIIRILVQKLRPPDIGKNDSSPYSRLAKSTLLLIP
       290        300        310        320        330        340        350

       369        379        389        399        409        419        429
LFGIHYTVFAFSPENVSKRERLVFELGLGSFQGFVVAVLYCFLNGEVQAEIKRKWRSWKVNRYFTMDFKH
****** **** ***     ****** ****************************** ****   *   *
LFGIHYVMFAFFPDNFKAQVKMVFELVVGSFQGFVVAILYCFLNGEVQAELRRKWRRWHLQGVLGWSSKS
       360        370        380        390        400        410        420

       439        449        459
RHPSLASSGVNGGTQLSILSKSSSQLRMSSLPADNLAT*
 **  ** *   ********* **  * **    ***
QHPWGGSNGATCSTQVSMLTRVSPSARRSSSFQAEVSLV
       430        440        450
```

FIG. 20

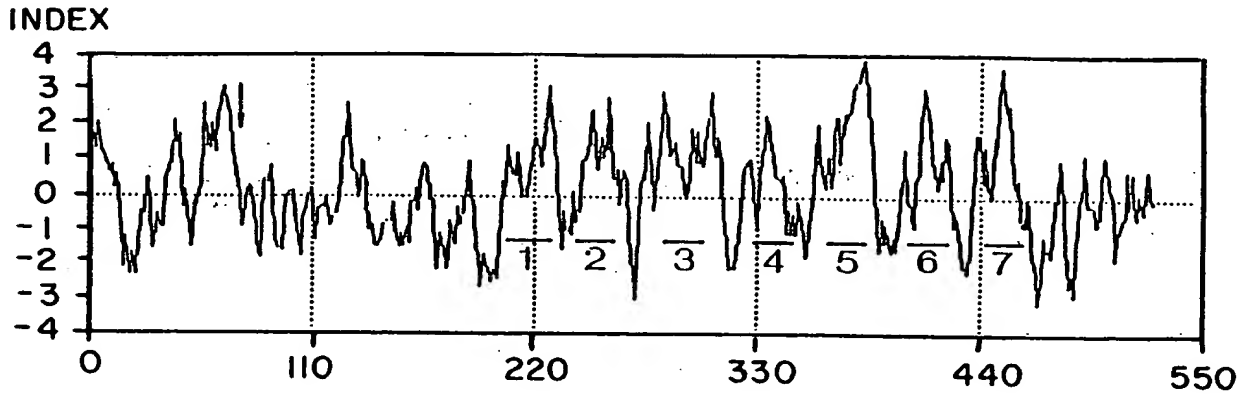

INDEX
4
3
2
1
0
-1
-2
-3
-4
1
2
3
4
5
6
7
0
110
220
330
440
550

FIG. 21

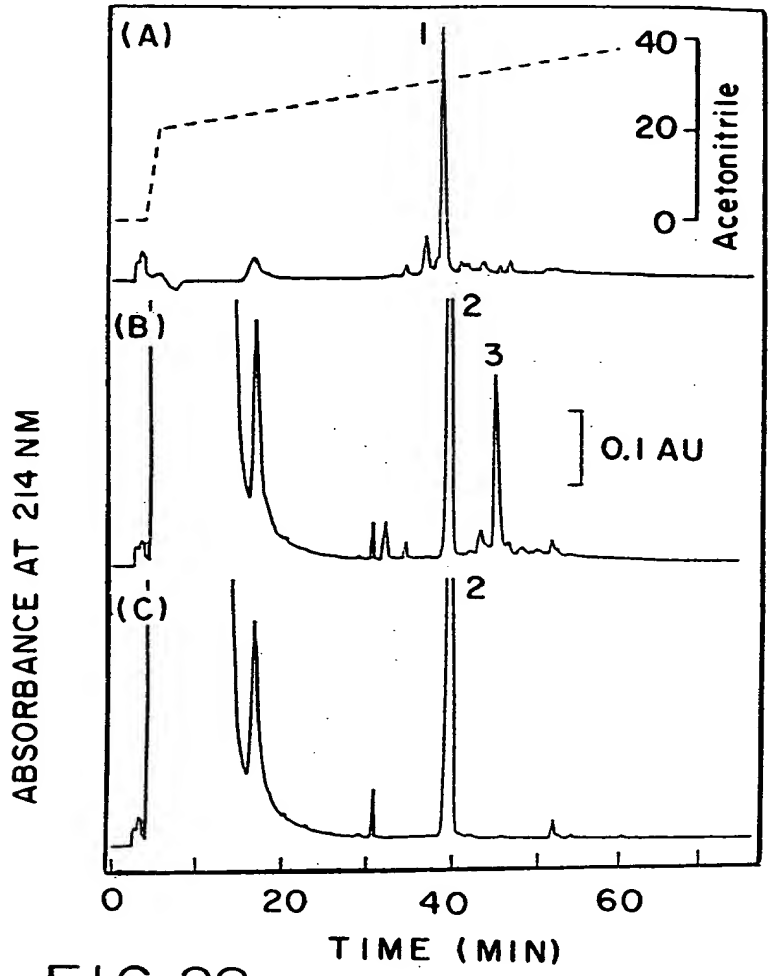

(A)
1
40
20
0
Acetonitrile
(B)
2
3
0.1 AU
(C)
2
ABSORBANCE AT 214 NM
0
20
40
60
TIME (MIN)

FIG. 28

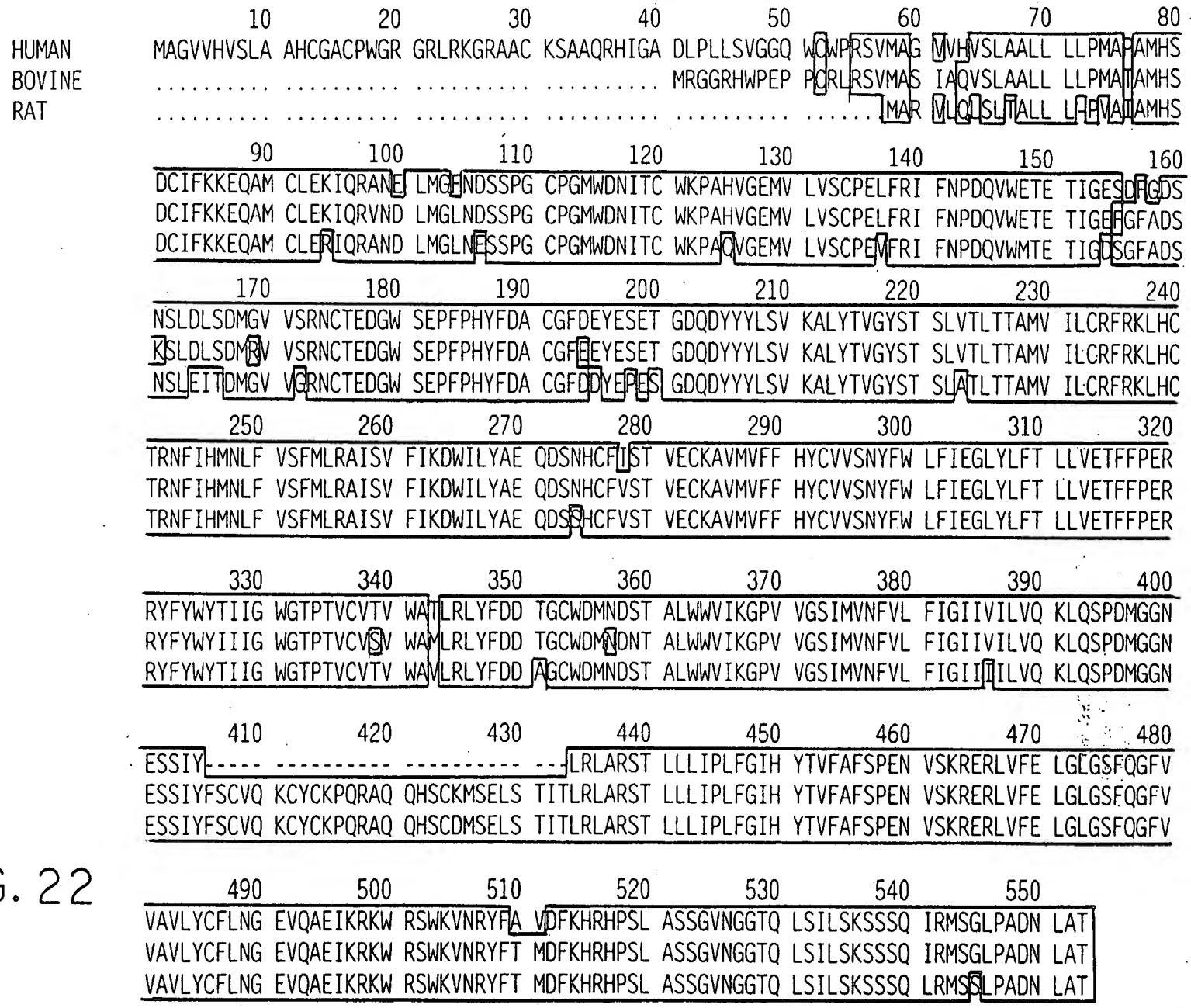

10 20 30 40 50 60 70 80
HUMAN MAGVVHVSLA AHCGACPWGR GRLRKGRAAC KSAAQRHIGA DLPLLSVGGQ WQWPRSVMAG VVHVSLAALL LLPMAPAMHS
BOVINE .... MRGGRHWPEP PQRLRSVMAS IAQVSLAALL LLPMATAMHS
RAT ....MAR VLQQSLTALL LHPVATAMHS
90 100 110 120 130 140 150 160
DCIFKKEQAM CLEKIQRANE LMGHNDSSPG CPGMWDNITC WKPAHVGEMV LVSCPELFRI FNPDQVWETE TIGESDFGDS
DCIFKKEQAM CLEKIQRVND LMGLNDSSPG CPGMWDNITC WKPAHVGEMV LVSCPELFRI FNPDQVWETE TIGEFGFADS
DCIFKKEQAM CLERIQRAND LMGLNESSPG CPGMWDNITC WKPAQVGEMV LVSCPEMFRI FNPDQVWMTE TIGDSGFADS
170 180 190 200 210 220 230 240
NSLDLSDMGV VSRNCTEDGW SEPFPHYFDA CGFDEYESET GDQDYYYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC
KSLDLSDMRV VSRNCTEDGW SEPFPHYFDA CGFEEYESET GDQDYYYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC
NSLEITDMGV VGRNCTEDGW SEPFPHYFDA CGFDDYEPES GDQDYYYLSV KALYTVGYST SLATLTTAMV ILCRFRKLHC
250 260 270 280 290 300 310 320
TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSNHCFIST VECKAVMVFF HYCVVSNYFW LFIEGLYLFT LLVETFFPER
TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSNHCFVST VECKAVMVFF HYCVVSNYFW LFIEGLYLFT LLVETFFPER
TRNFIHMNLF VSFMLRAISV FIKDWILYAE QDSSHCFVST VECKAVMVFF HYCVVSNYFW LFIEGLYLFT LLVETFFPER
330 340 350 360 370 380 390 400
RYFYWYTIIG WGTPTVCVTV WAVLRLYFDD TGCWDMNDST ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGGN
RYFYWYIIIG WGTPTVCVSV WAMLRLYFDD TGCWDMNDNT ALWWVIKGPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGGN
RYFYWYTIIG WGTPTVCVTV WAMLRLYFDD AGCWDMNDST ALWWVIKGPV VGSIMVNFVL FIGIITILVQ KLQSPDMGGN
410 420 430 440 450 460 470 480
ESSIY----- ---------- ---------- ---LRLARST LLLIPLFGIH YTVFAFSPEN VSKRERLVFE LGLGSFQGFV
ESSIYFSCVQ KCYCKPQRAQ QHSCKMSELS TITLRLARST LLLIPLFGIH YTVFAFSPEN VSKRERLVFE LGLGSFQGFV
ESSIYFSCVQ KCYCKPQRAQ QHSCDMSELS TITLRLARST LLLIPLFGIH YTVFAFSPEN VSKRERLVFE LGLGSFQGFV
490 500 510 520 530 540 550
VAVLYCFLNG EVQAEIKRKW RSWKVNRYFA VDFKHRHPSL ASSGVNGGTQ LSILSKSSSQ IRMSGLPADN LAT
VAVLYCFLNG EVQAEIKRKW RSWKVNRYFT MDFKHRHPSL ASSGVNGGTQ LSILSKSSSQ IRMSGLPADN LAT
VAVLYCFLNG EVQAEIKRKW RSWKVNRYFT MDFKHRHPSL ASSGVNGGTQ LSILSKSSSQ LRMSSLPADN LAT

FIG. 22

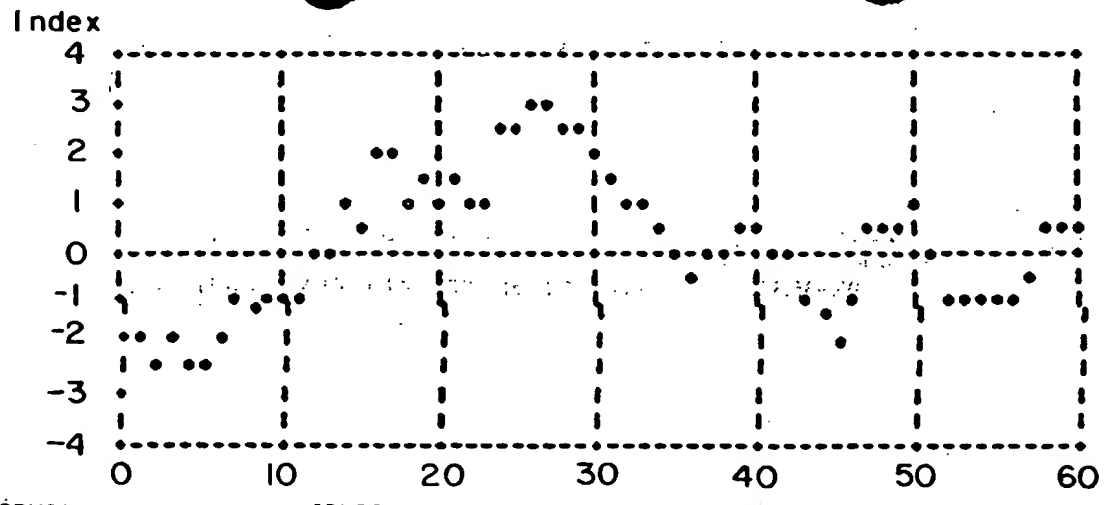


FIG.23A

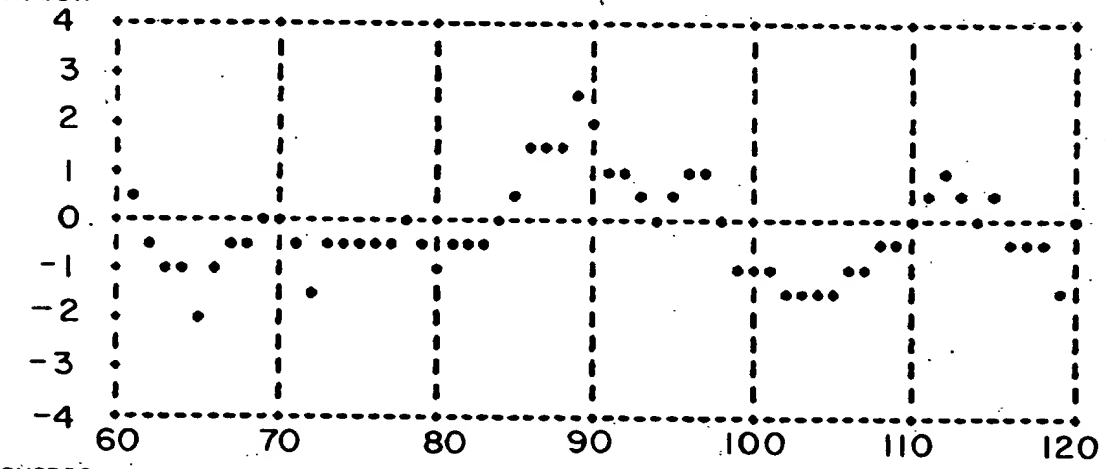


FIG.23B

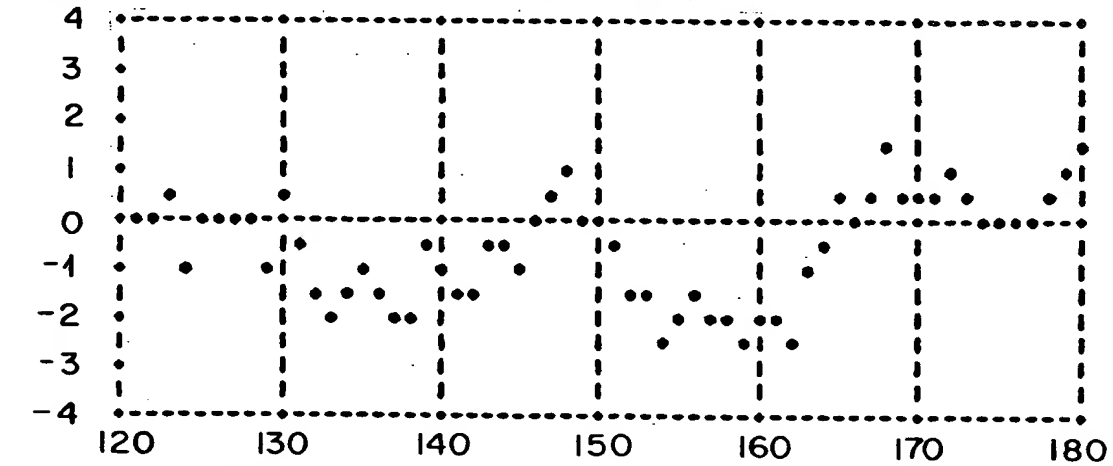


FIG.23C

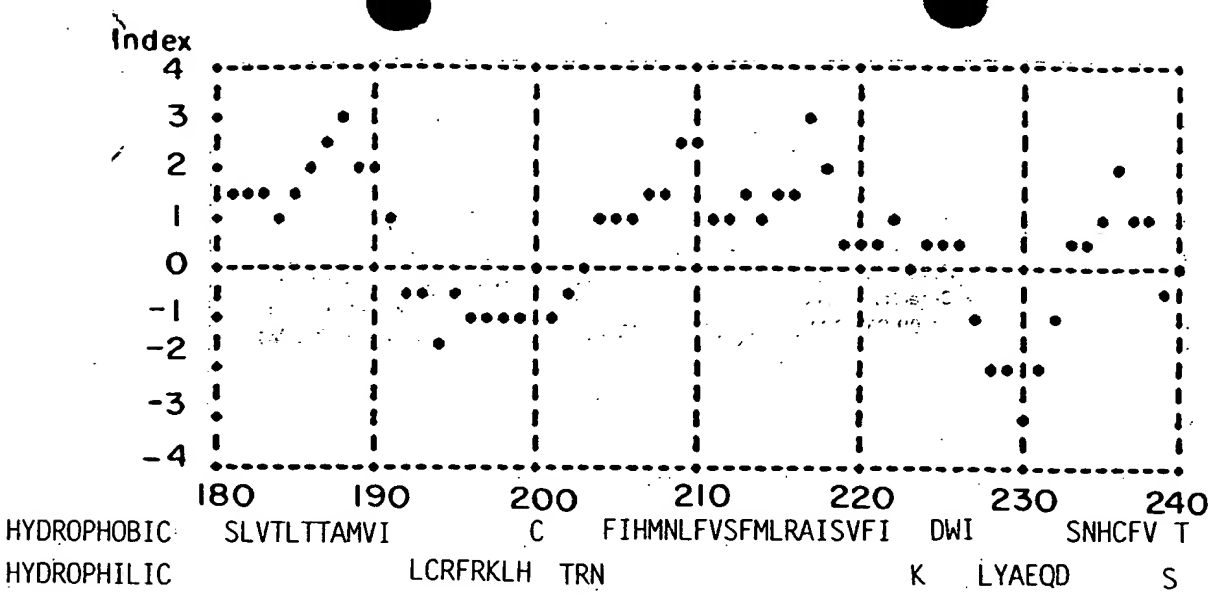


FIG. 23D

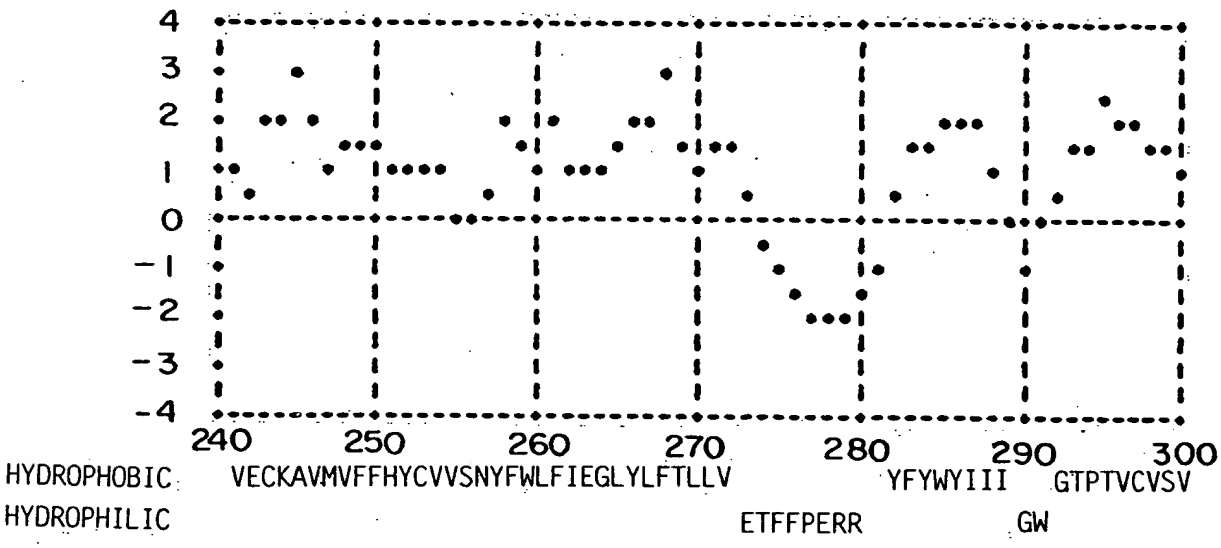


FIG. 23E

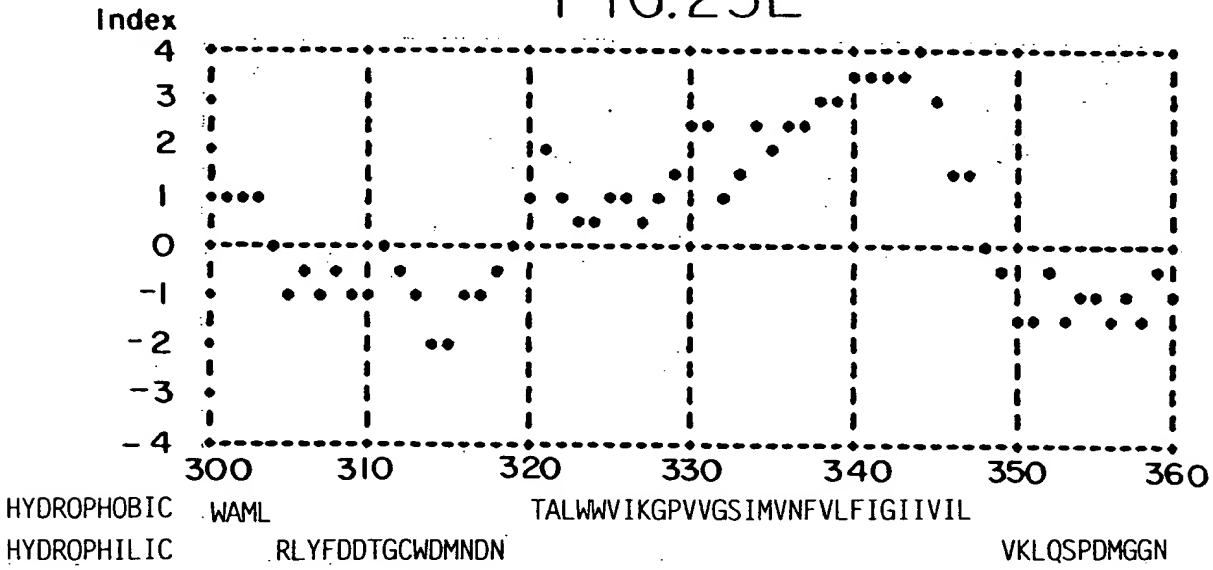


FIG. 23F

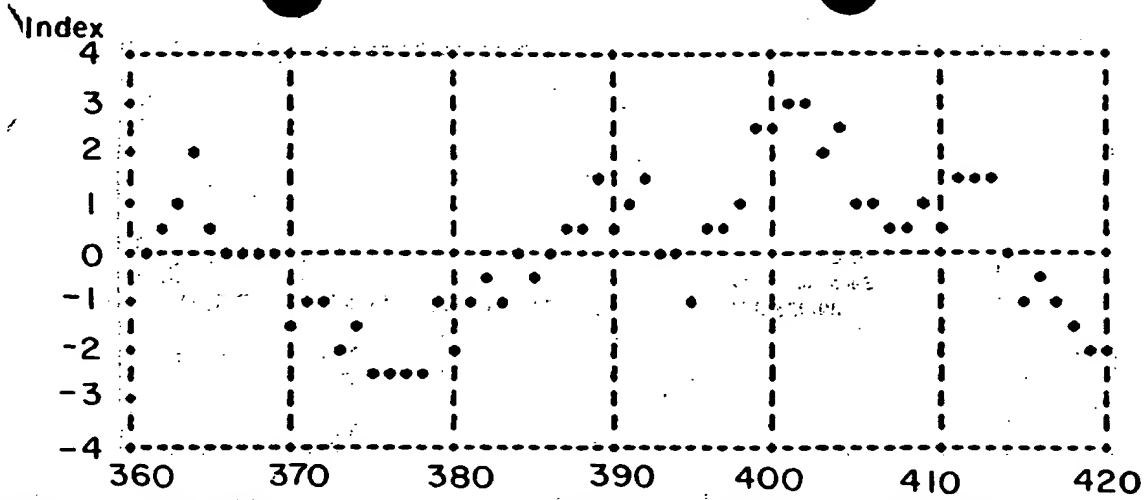


FIG.23G

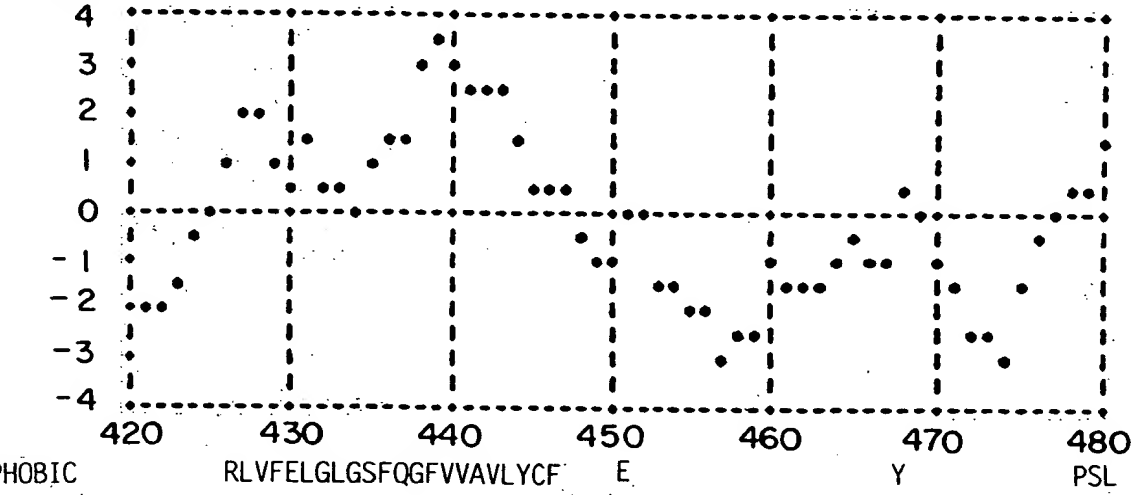


FIG.23H

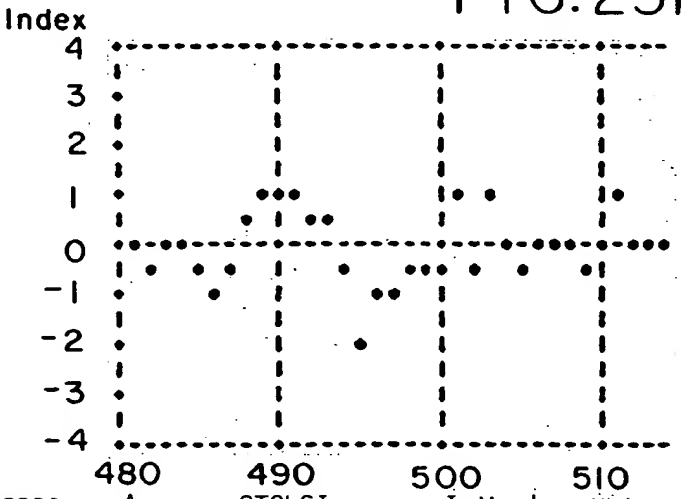


FIG. 23I

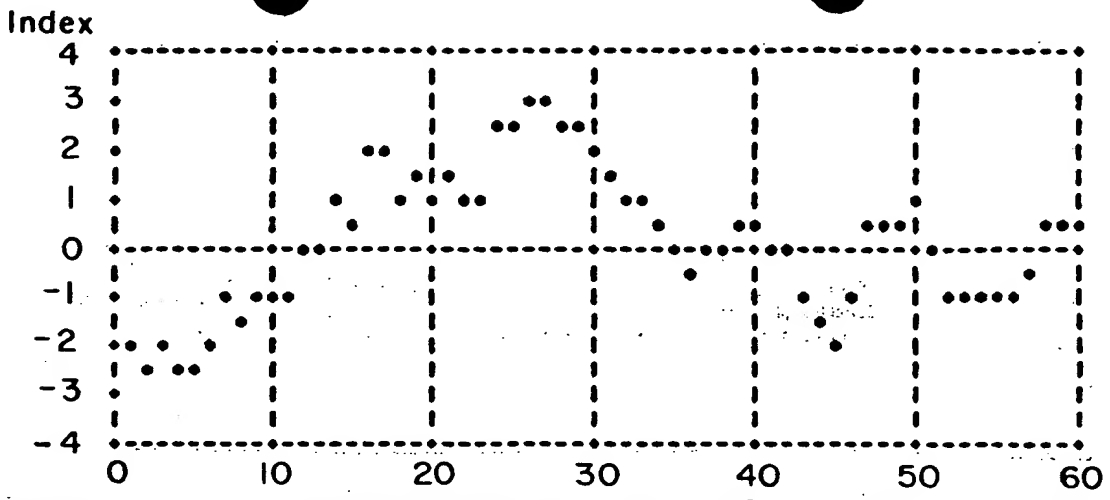


FIG. 24A

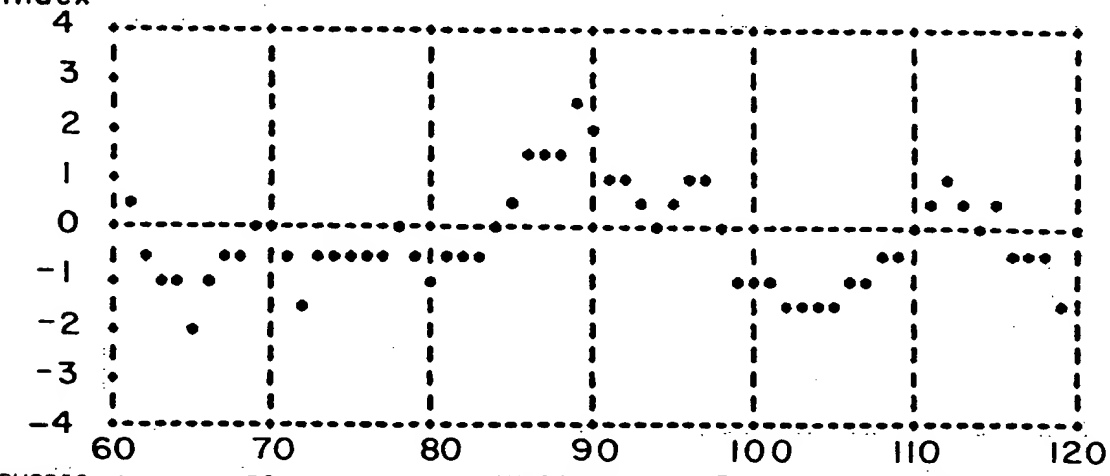


FIG. 24B

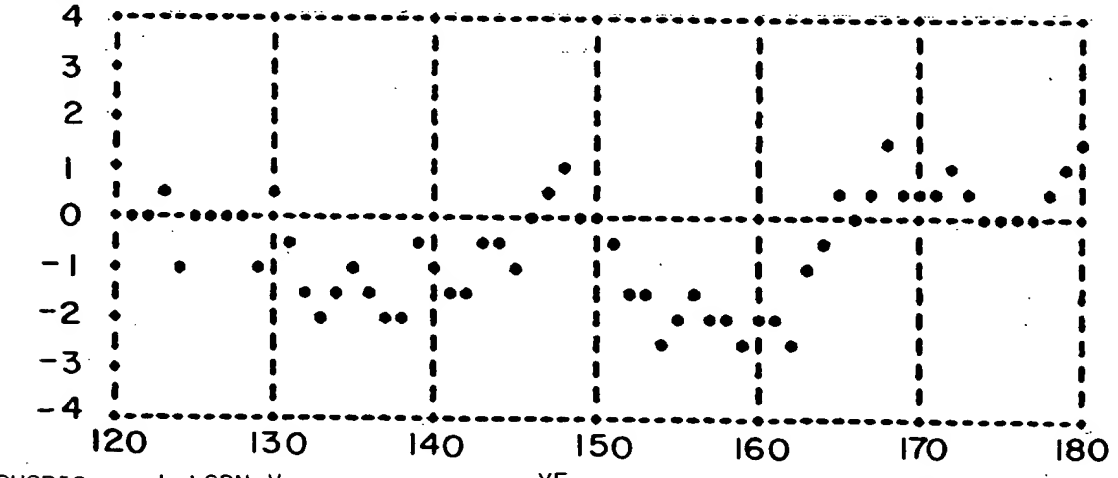


FIG. 24C

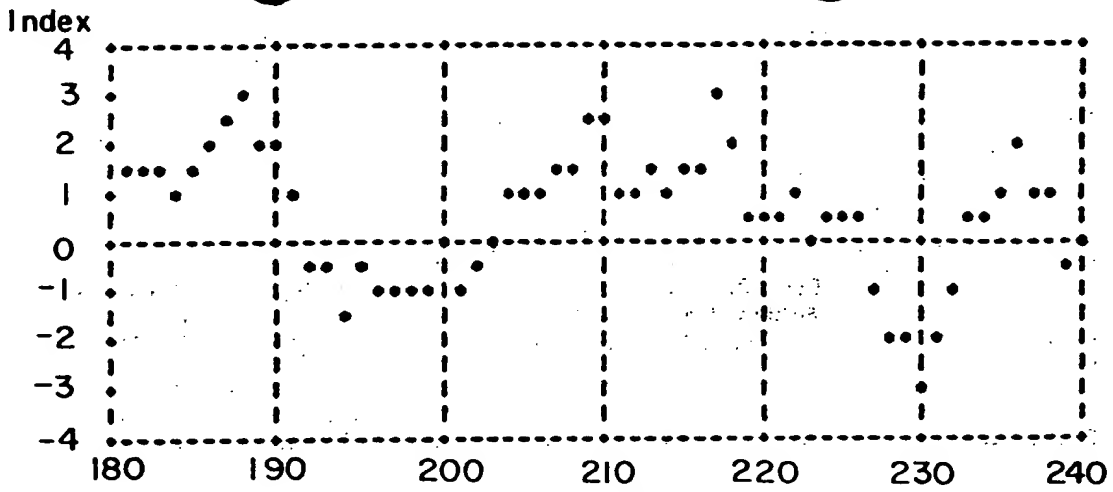


FIG. 24D

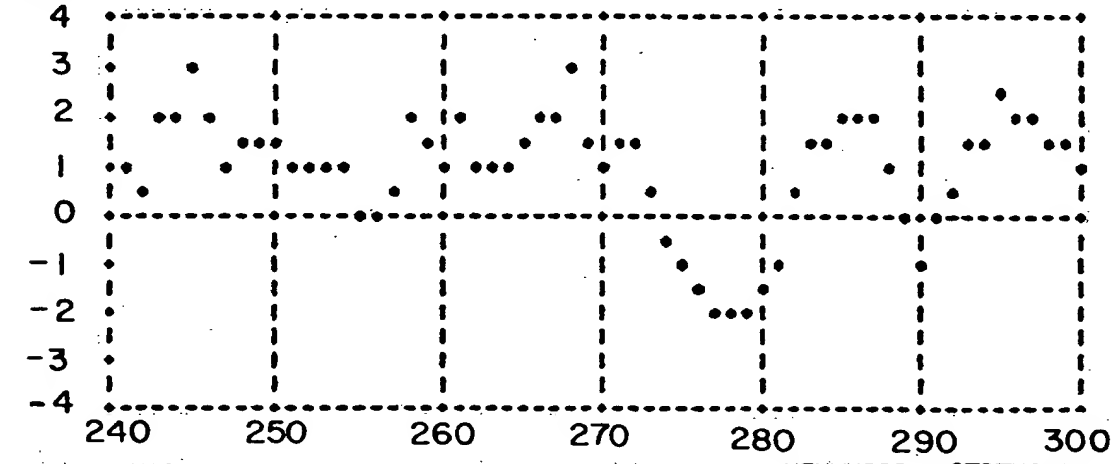


FIG. 24E

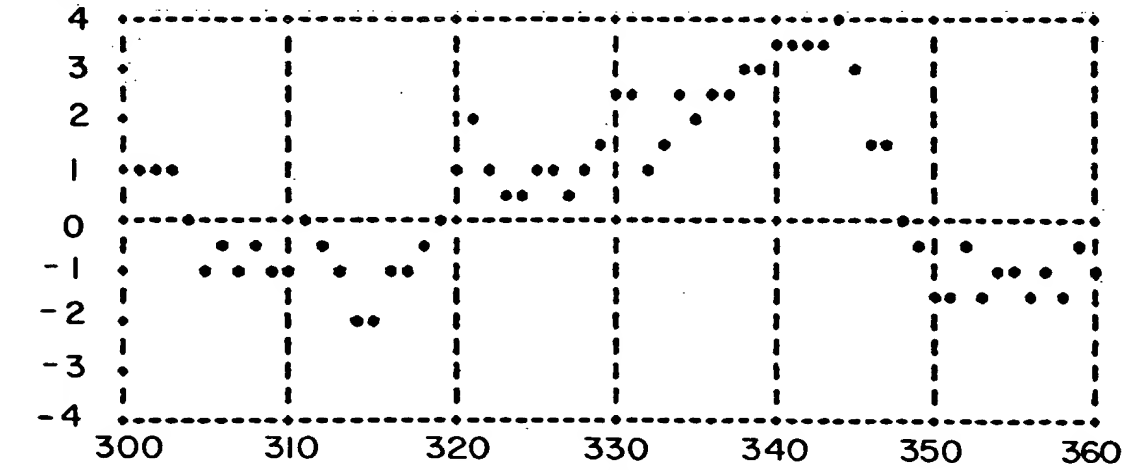


FIG. 24F

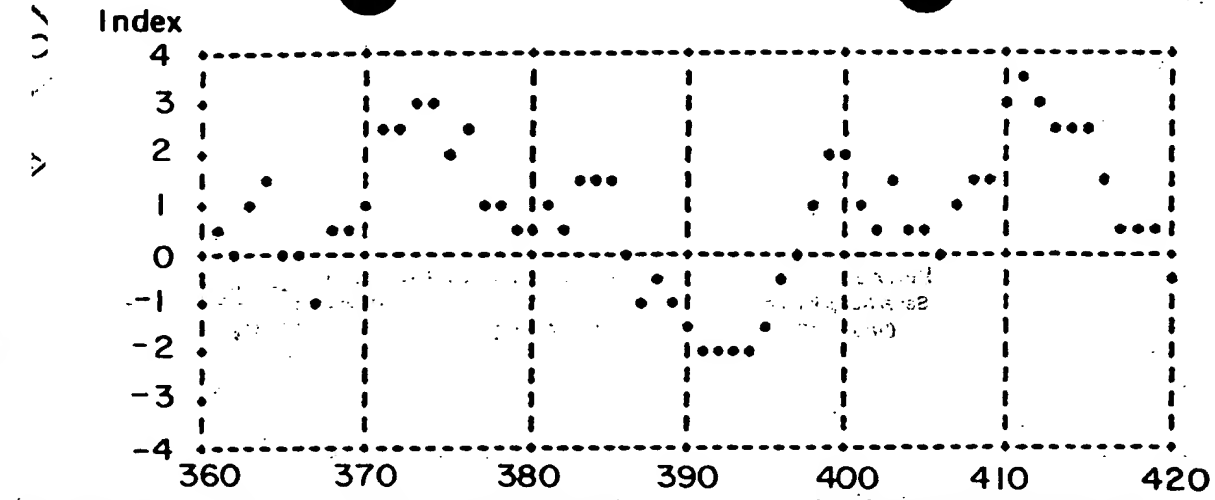


FIG. 24G

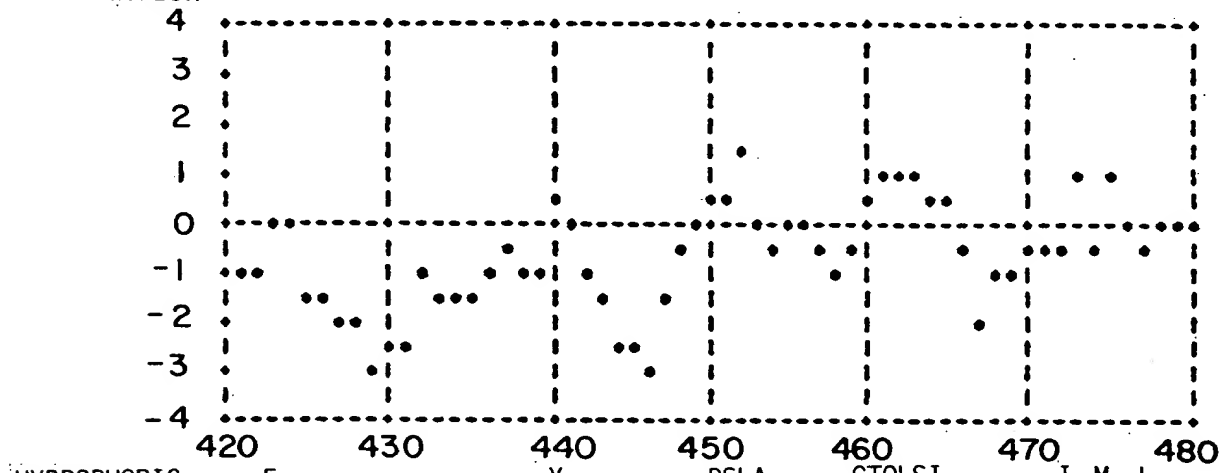


FIG. 24H

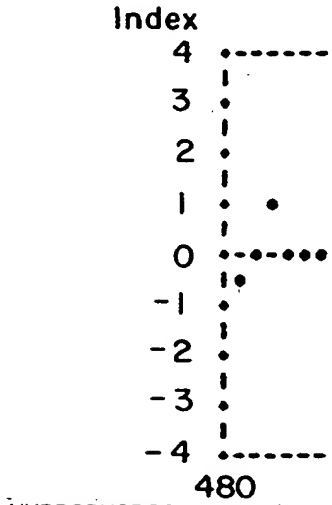
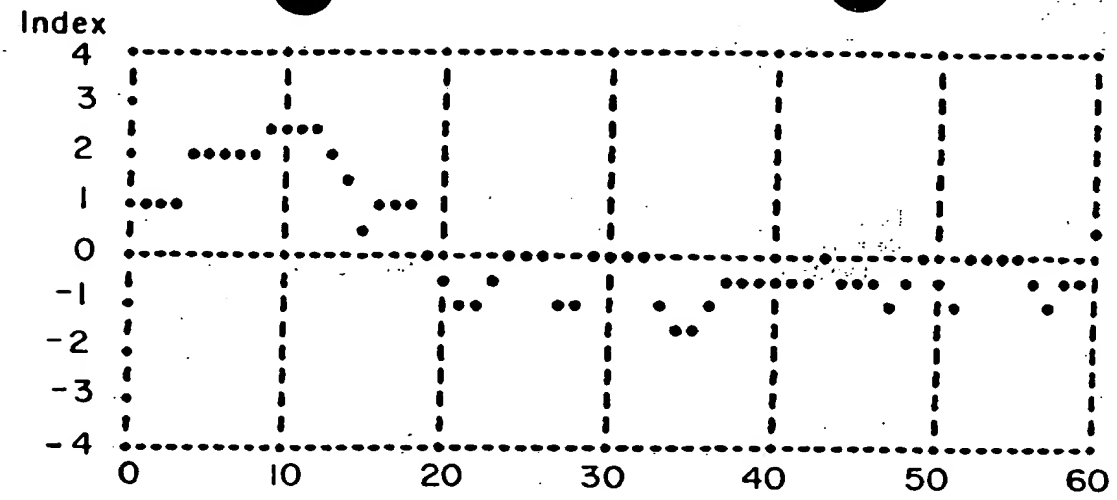


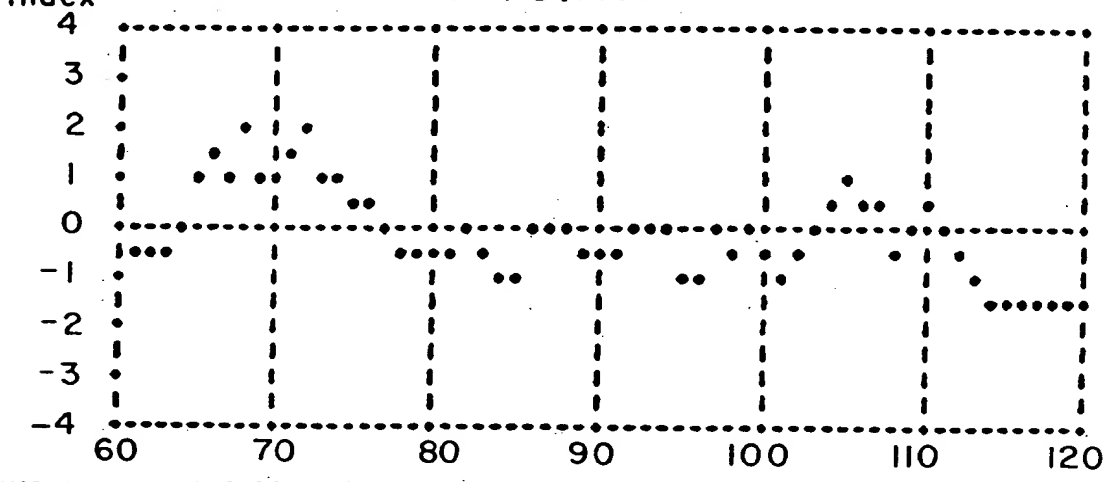
FIG. 24I



HYDROPHOBIC MARVLQLSLTALLLPVAIA I

HYDROPHILIC MHSDCIFKKEQANCLERIQRANDLMGLNESSPGCPMWDN

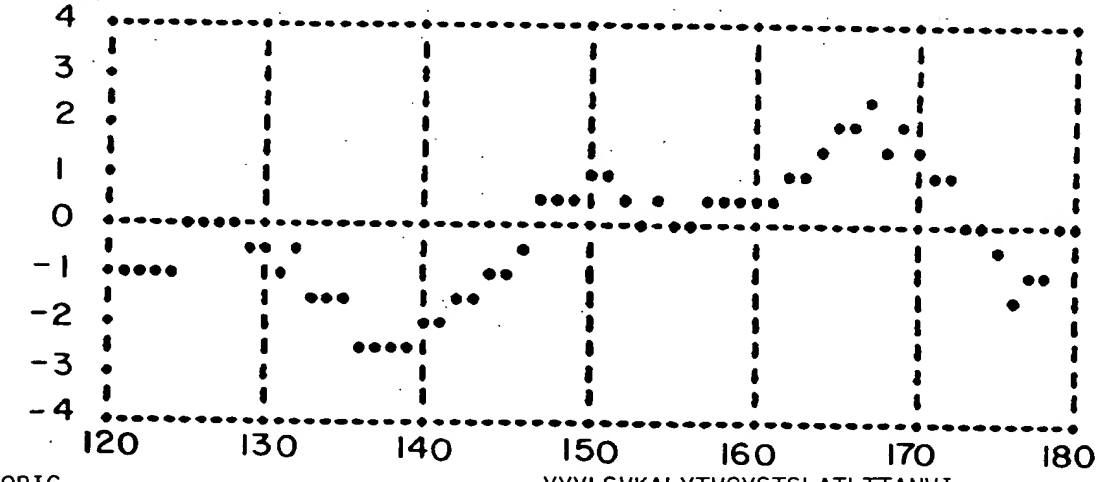
FIG.25A



HYDROPHOBIC PAQVGENVLVSC I QV F SLEI DN

HYDROPHILIC TCWK FEVFR FNPD WMTETIGDSG ADSN T GVVGRNCTED

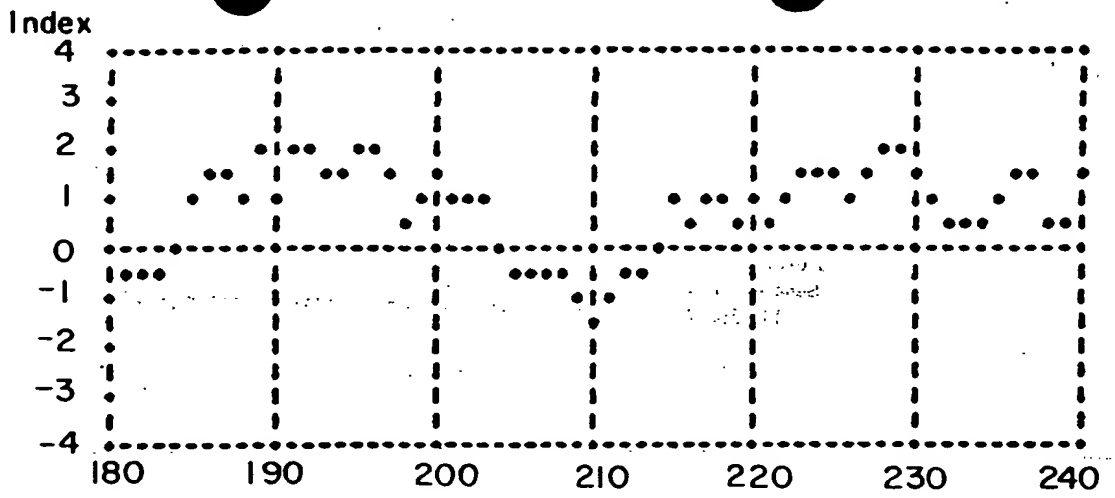
FIG.25B



HYDROPHOBIC YYYLSVKALYTVGYSTSLATLTTANVI

HYDROPHILIC GWSEPFPHYFDACGFDDYEPESGDQD LCRFRKL

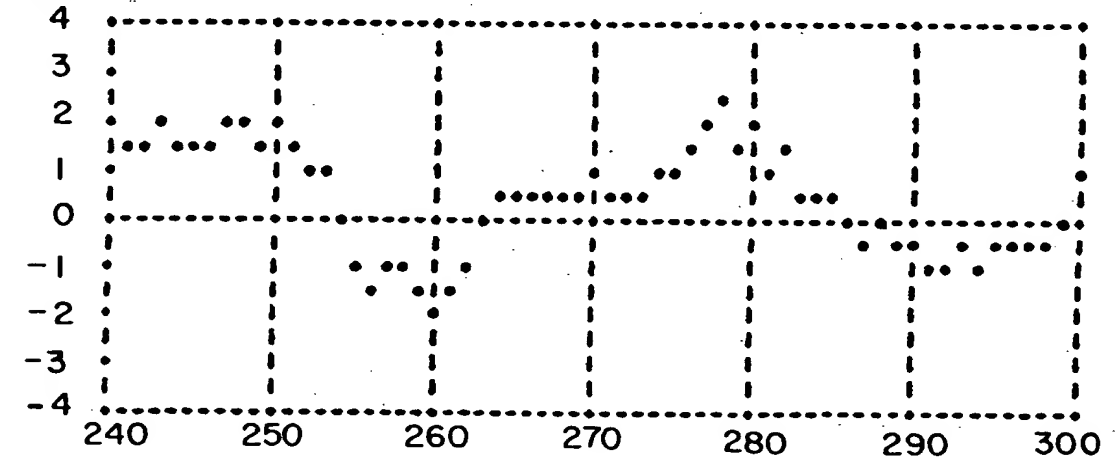
FIG.25C



HYDROPHOBIC RNFIHMNLFVSFMLRAISVFI SSHCFVSTVECKAVMVFFHYCVVSNY

HYDROPHILIC HCT KDWILYAEQD

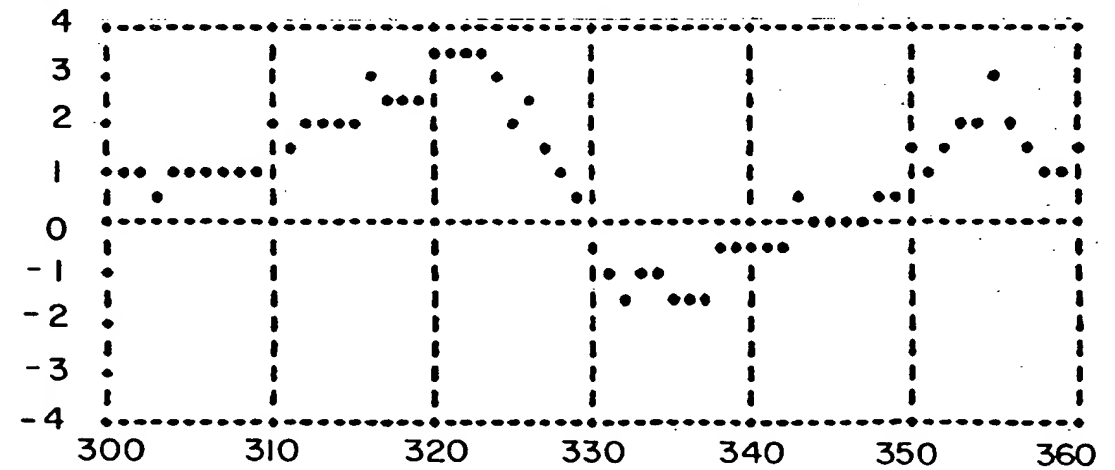
FIG.25D



HYDROPHOBIC FWLFIEGLYLFTL RYFYWYTIIGWGTPTVCVTVWAV L D

HYDROPHILIC LVETFFPER LR YFDDAGCWDMN

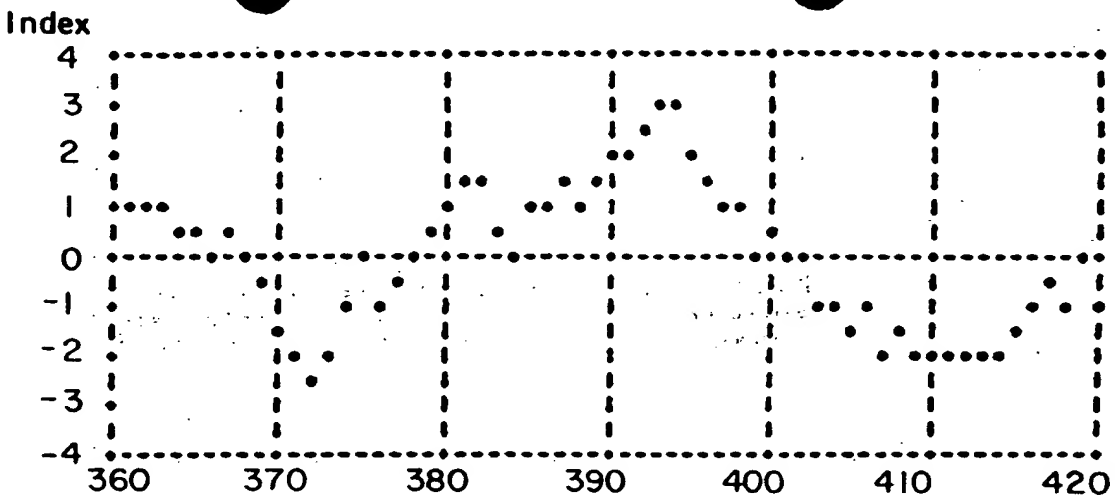
FIG.25E



HYDROPHOBIC STALWWVIKGPVVGSIMVMVLFIGIIII KSSIYLRLARSTLLLIPL

HYDROPHILIC LVQKLQSPDMGGN

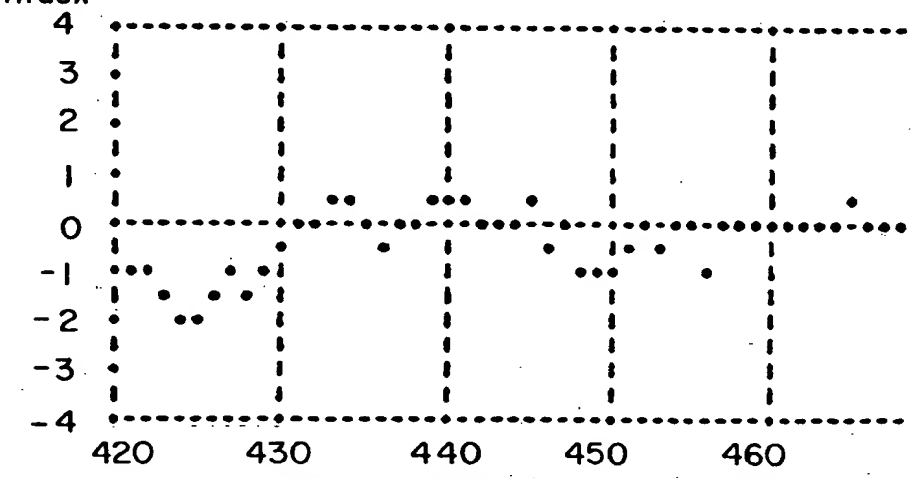
FIG.25F



HYDROPHOBIC FGIHTYVF ERLVEFELGLGSFQGFVVAVLYC

HYDROPHILIC AFSPENVSKR FLNGEVQAEIKKKWRSWKVN

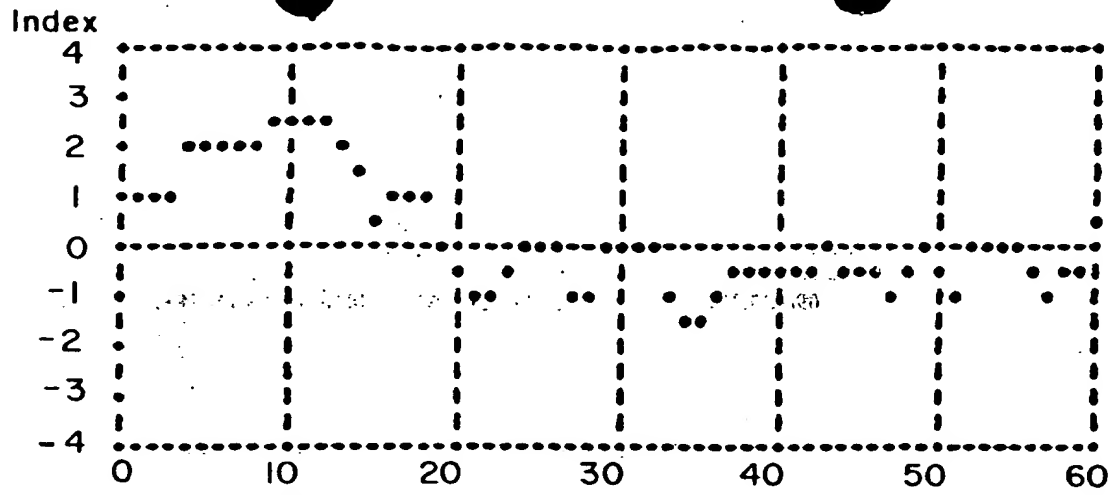
FIG. 25G



HYDROPHOBIC HPSL VNGGTQL I QL MSSL NLA •

HYDROPHILIC RYFTMDFKHR ASSG S LSKSSS R PAD T

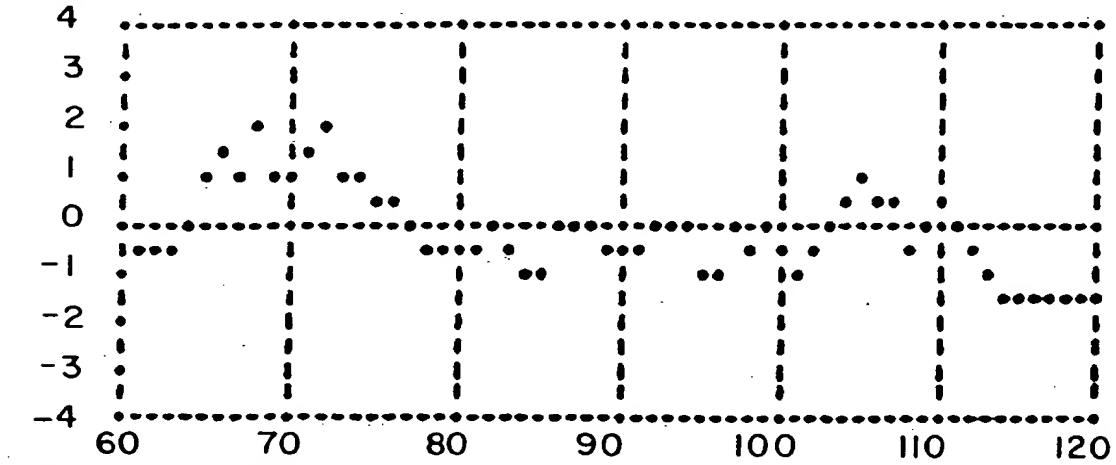
FIG. 25H



HYDROPHOBIC MARVLQLSLTALLLPVAIA I

HYDROPHILIC MHSDCIFKKEQANCLERIQRANDLMGLNESSPGCPGMWDN

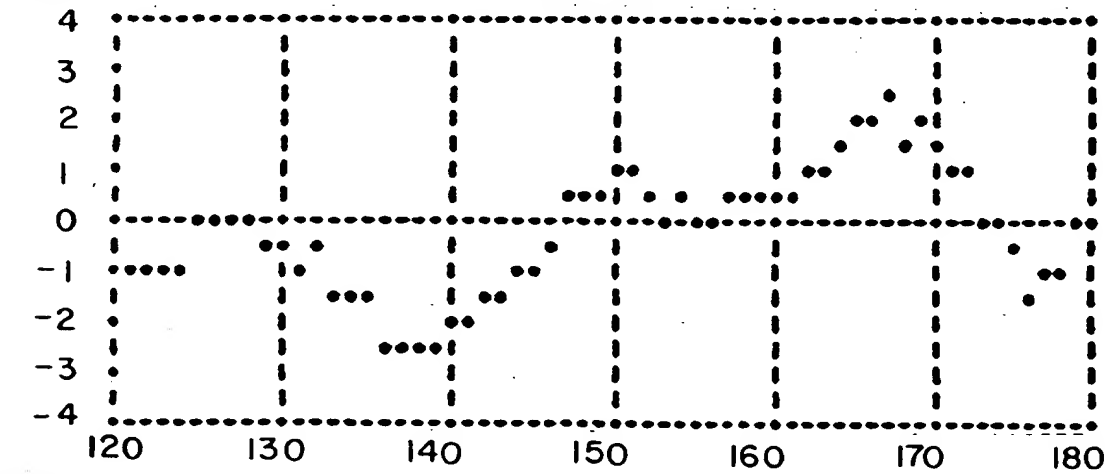
FIG.26A



HYDROPHOBIC PAQVGENVLVSC I QV F SLEI DM

HYDROPHILIC TCWK PEVFR FNPD WNTETIGDSG ADSN T GVVGRNCTKD

FIG.26B



HYDROPHOBIC YYYLSVKALYYVGYSTSLATLTTANVI

HYDROPHILIC GWSEPFPHYFDACGFDDYEPESGDQD LCAFRKL

FIG.26C

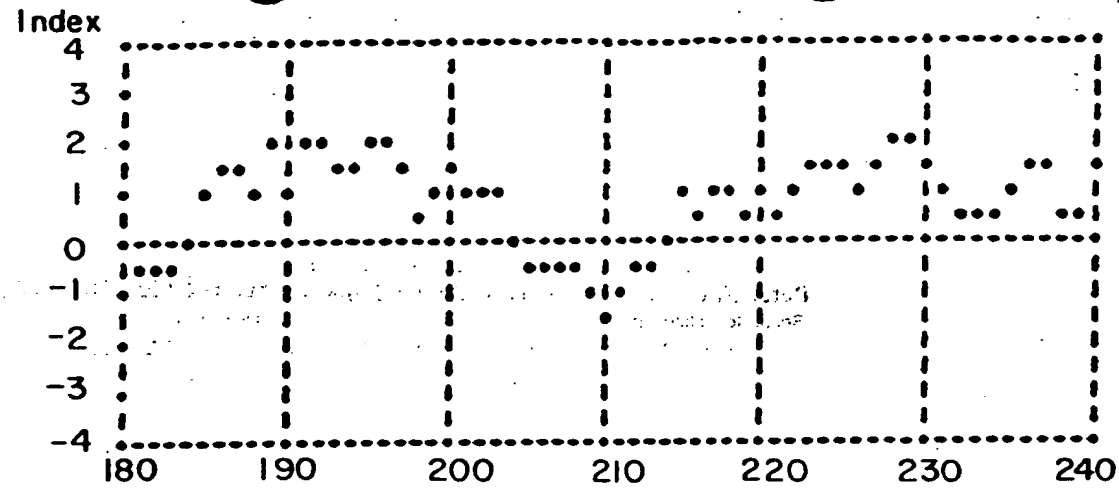


FIG.26D

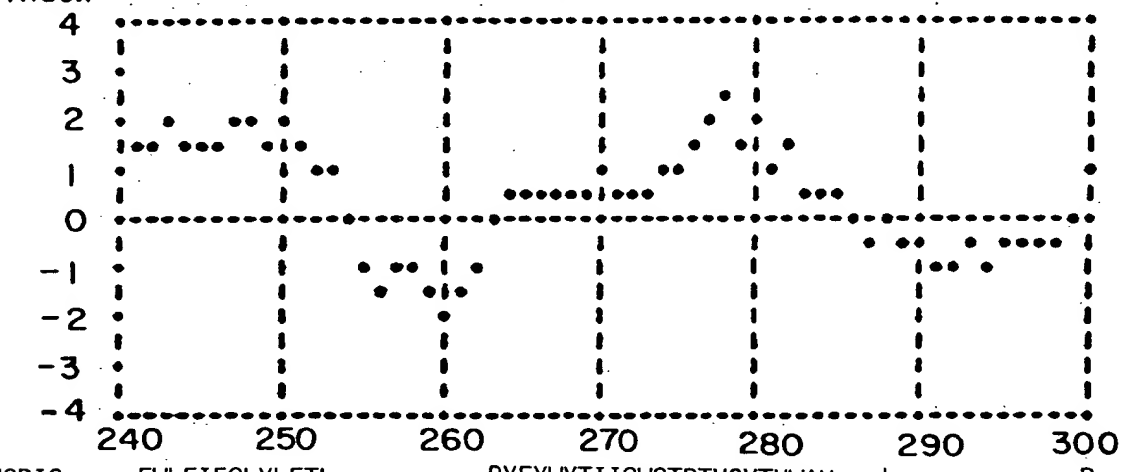


FIG.26E

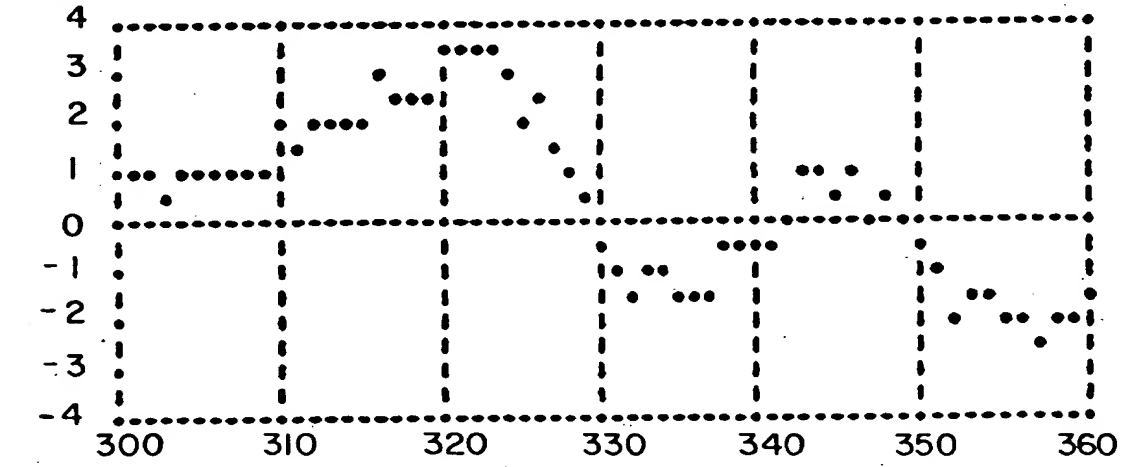
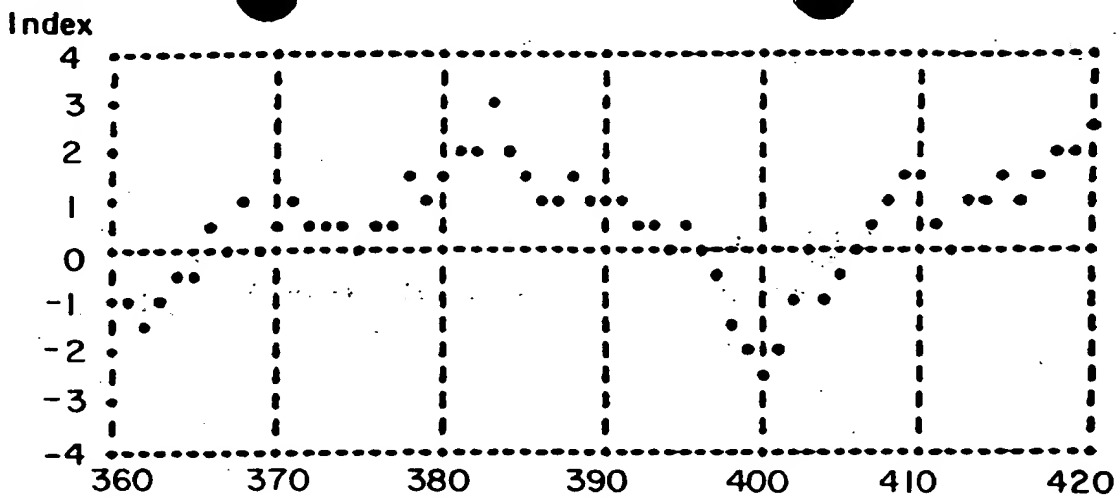
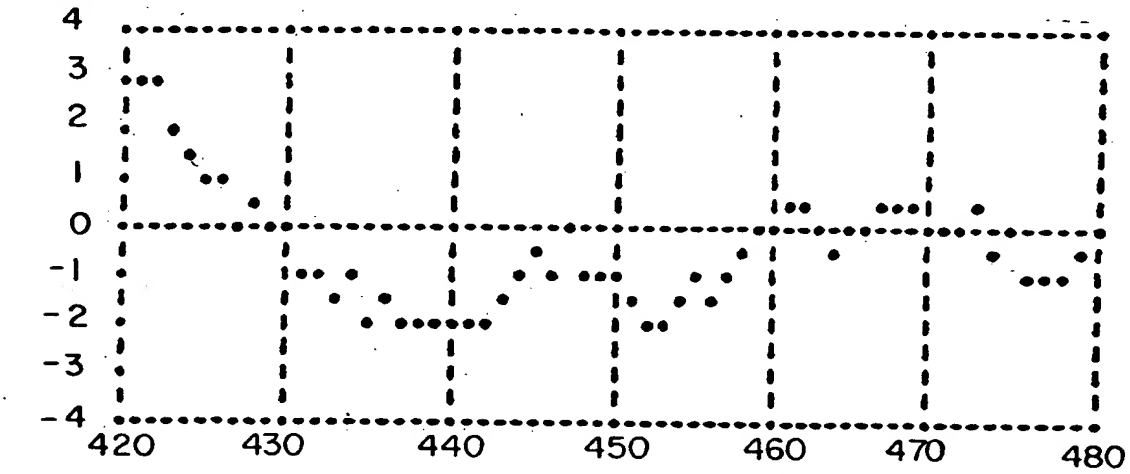


FIG.26F



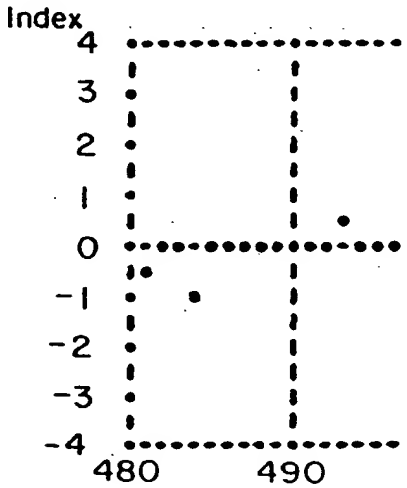
HYDROPHOBIC C MSELSTITLRLARSTILLLIPLFGIMYTVF ERLVFELGLGSFQG
HYDROPHILIC AQQHS K AFSPENVSKR

FIG.26G



HYDROPHOBIC FWVAVLYC MPSL VMGGTQL I
HYDROPHILIC FLNGEVQAEIKRKWRSWKVNRYFTNDFEMR ASSG S LSRSS

FIG.26H



HYDROPHOBIC QL MSSL NLA •
HYDROPHILIC S R PAD T

FIG.26I

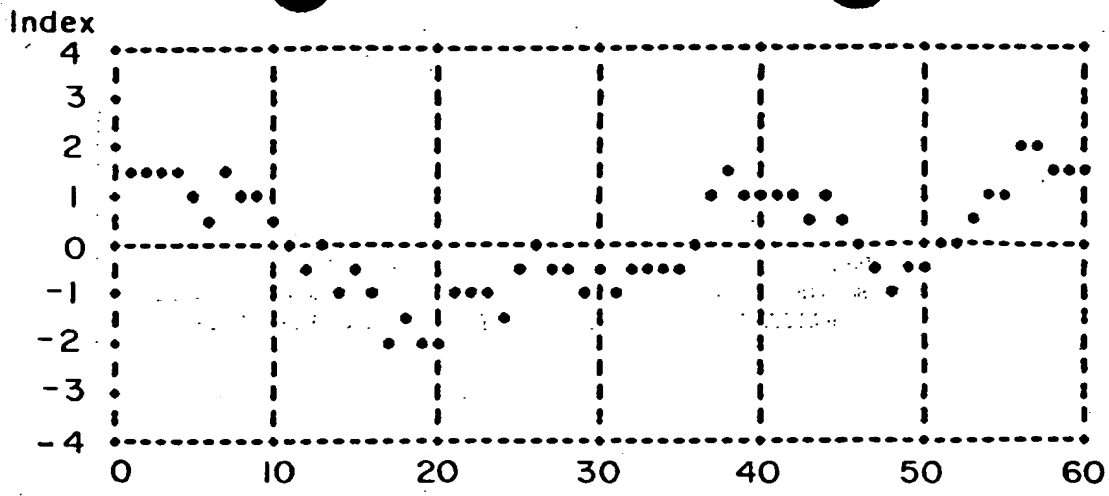


FIG.27A

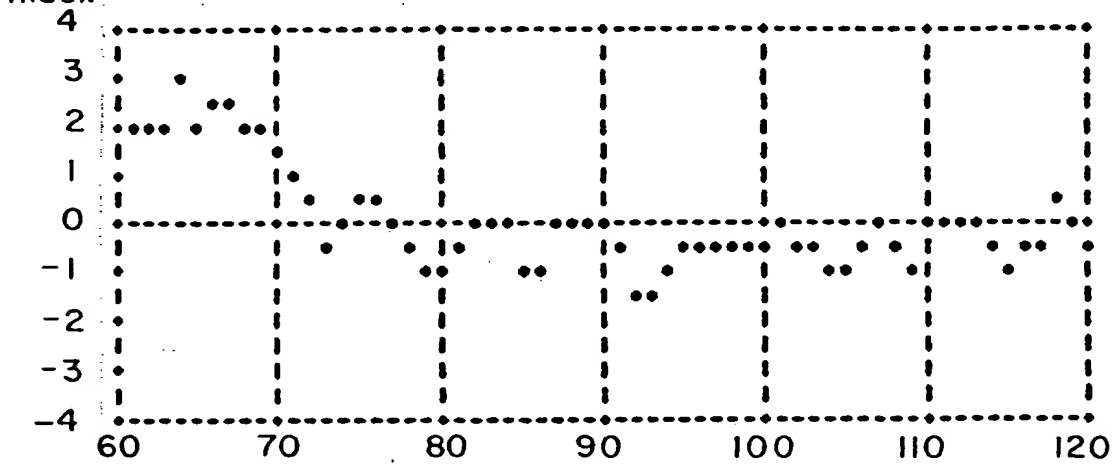


FIG.27B

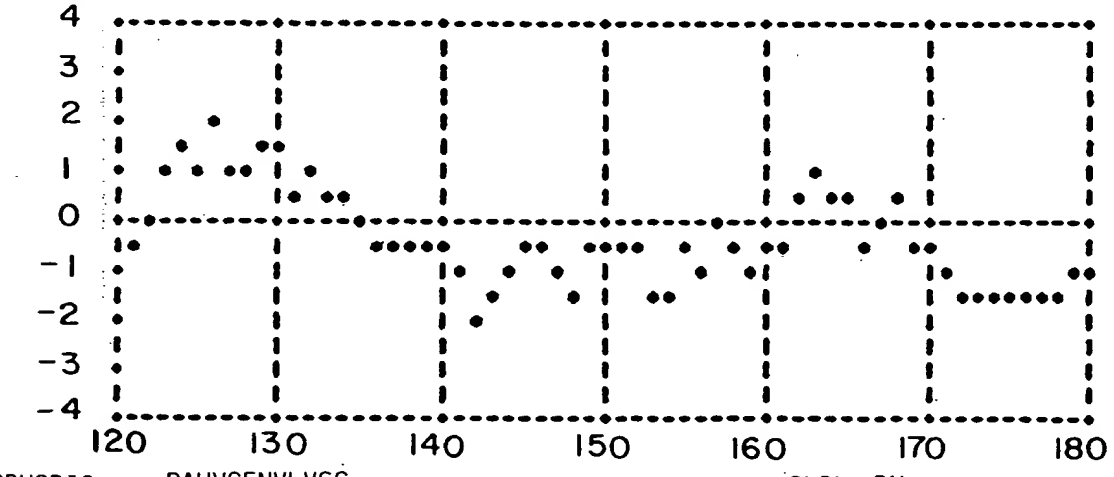
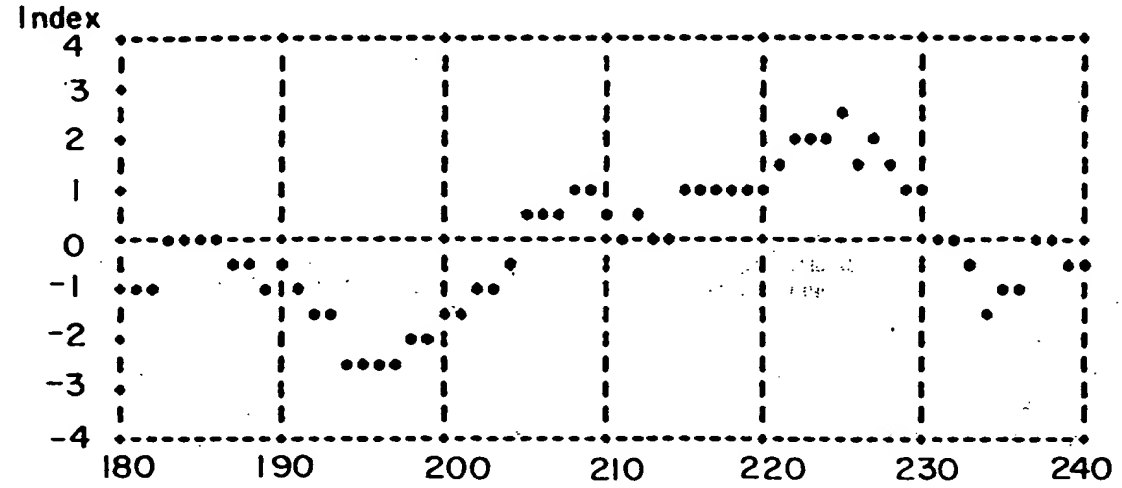


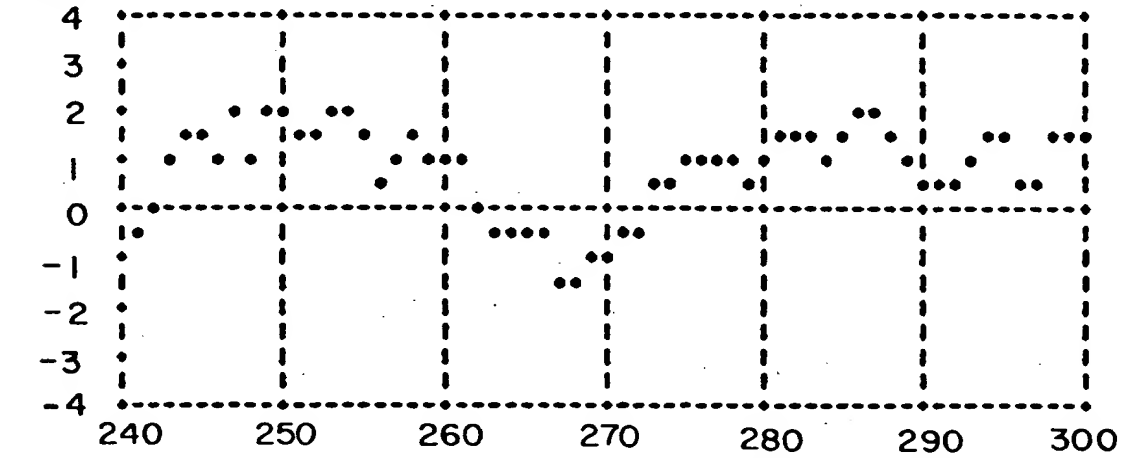
FIG.27C



HYDROPHOBIC YYYLSVKALYTVGYSTSLVTLTTAMVI

HYDROPHILIC SEPFPHYFDACGFDEYESETGDQD LCRFRKLHC

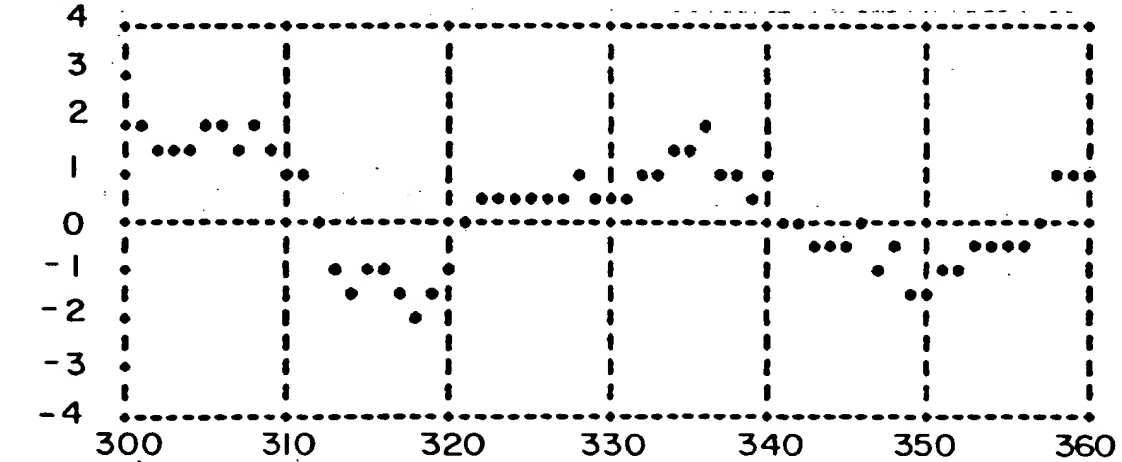
FIG.27D



HYDROPHOBIC RNFIHMNLFVSFMLRAISVFI SNHCFISTVECKAVMVFFHYCVVSNYFW

HYDROPHILIC T KDWILYAEQD

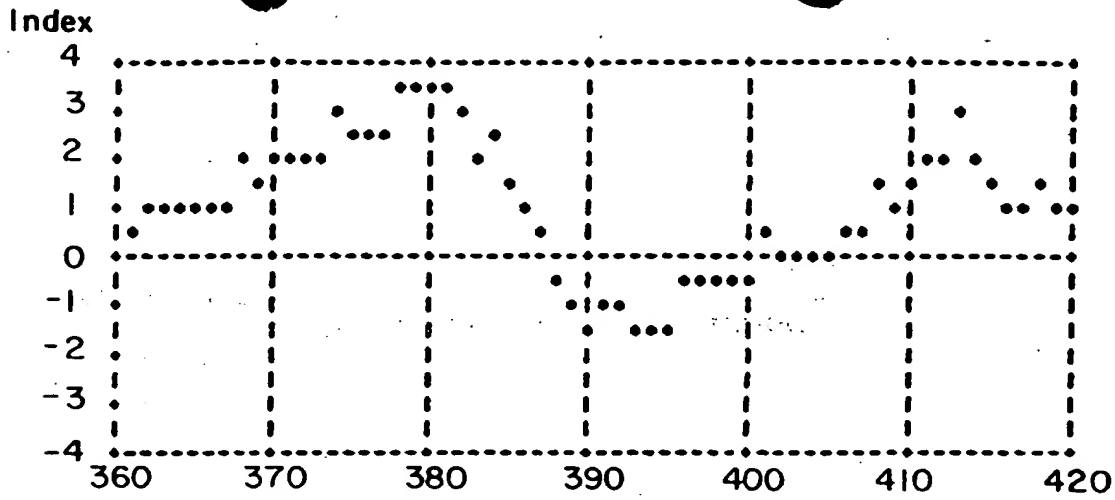
FIG.27E



HYDROPHOBIC LFIEGLYLFTL RYFYWYTIIGWGTPTVCVTVW DST

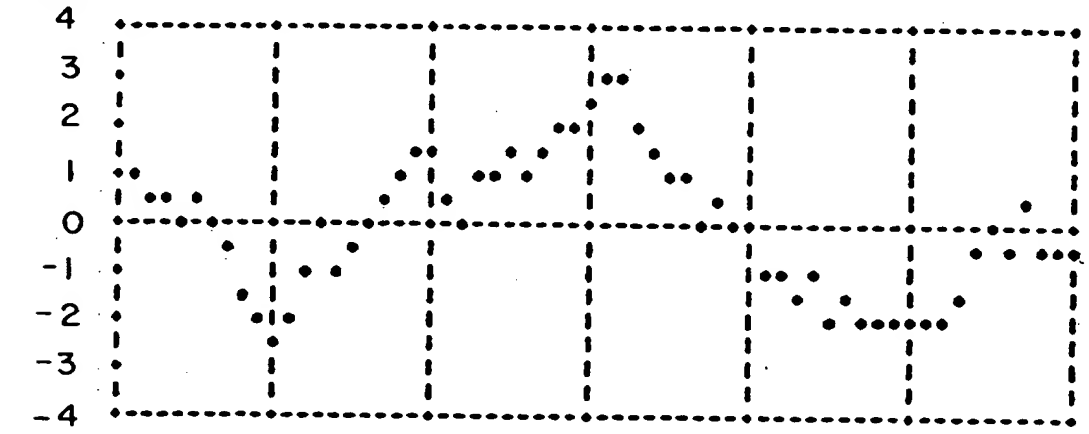
HYDROPHILIC LVETFFPER ATLRLYFDDTGCWDMN

FIG.27F



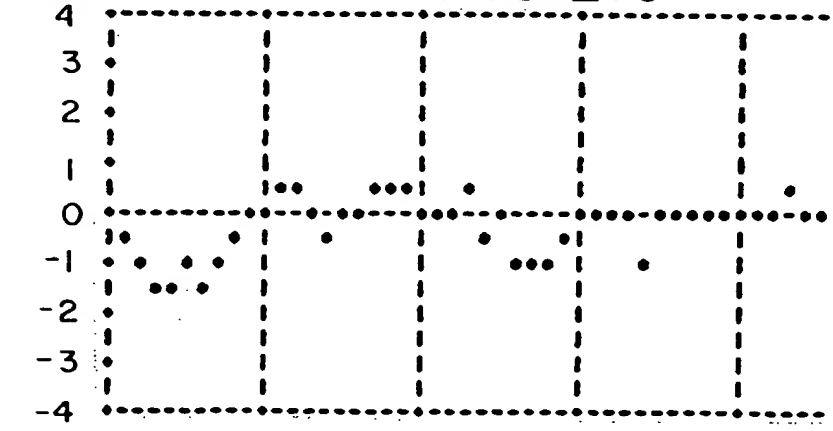
HYDROPHOBIC ALWWVIKGPVVGSIMVNFVLFIGIIVI ESSIYLRLARSTLLLIPLFG
HYDROPHILIC LVQKLQSPDMGGN

FIG.27G



HYDROPHOBIC IHYTVF ERLVFELGLGSFQGFVVAVLYC V
HYDROPHILIC AFSPENVSKR FLNGEVQAEIKRKWRSWK NRY

FIG.27I



HYDROPHOBIC HPSL VNGGTQL I QI MSGL NLA
HYDROPHILIC FAVDFKHR ASSG S LSKSSS R PAD T

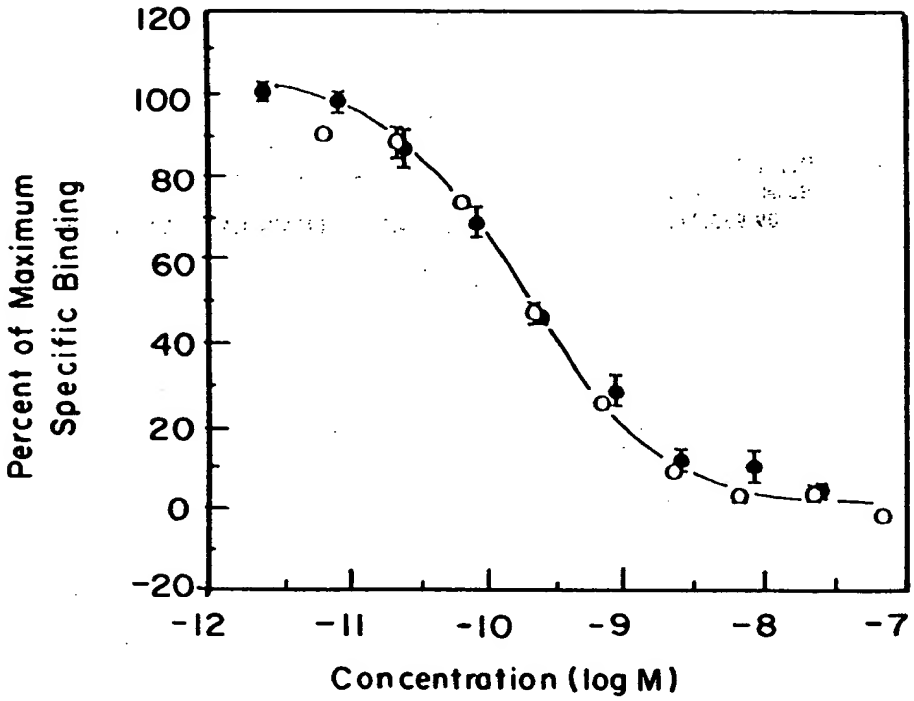

120
100
80
60
40
20
0
-20
-12
-11
-10
-9
-8
-7
Percent of Maximum
Specific Binding
Concentration (log M)

FIG. 29

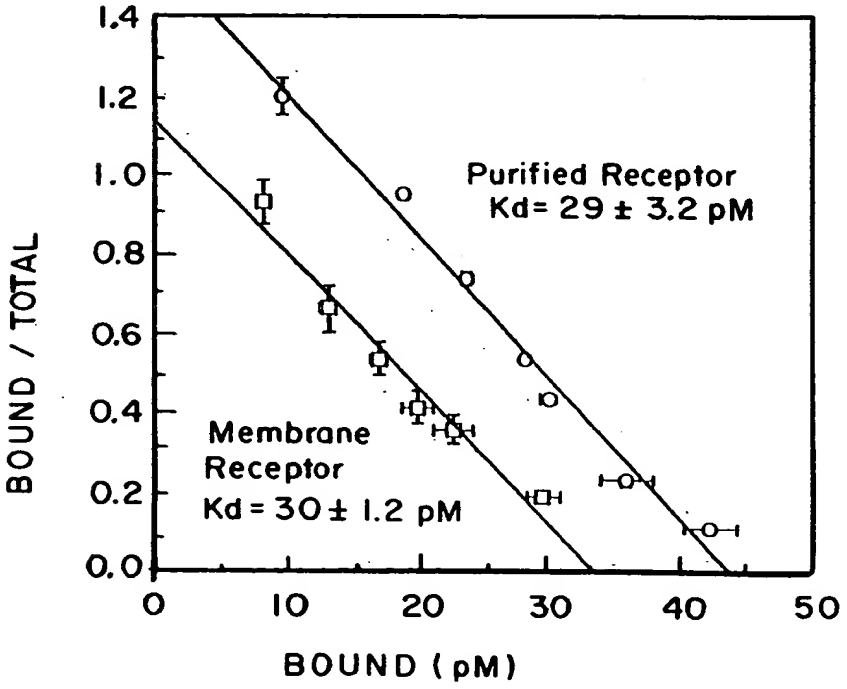

1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
BOUND / TOTAL
BOUND (pM)
Purified Receptor
Kd= 29 ± 3.2 pM
Membrane
Receptor
Kd = 30 ± 1.2 pM

FIG. 30

FIG. 31

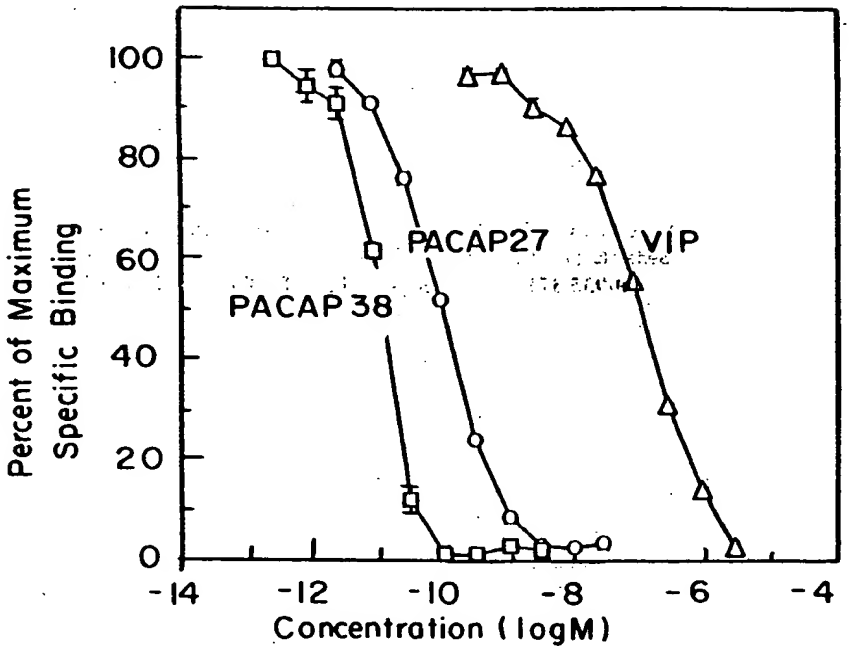


FIG. 33

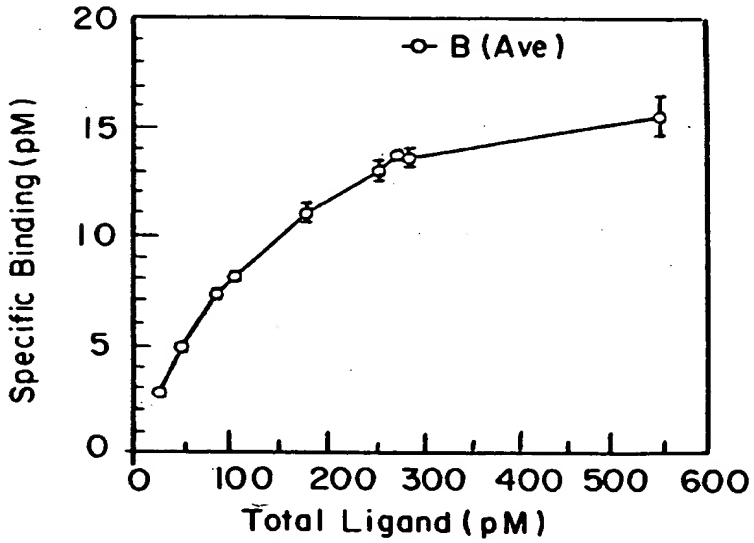


FIG. 34

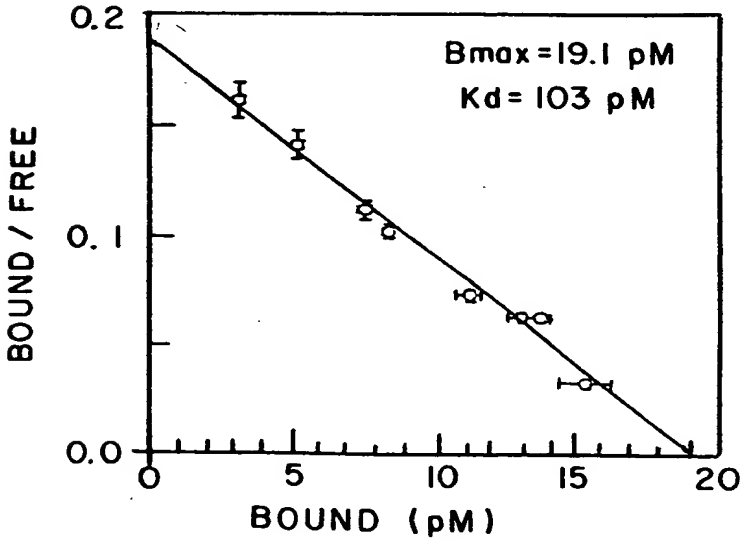


FIG. 35

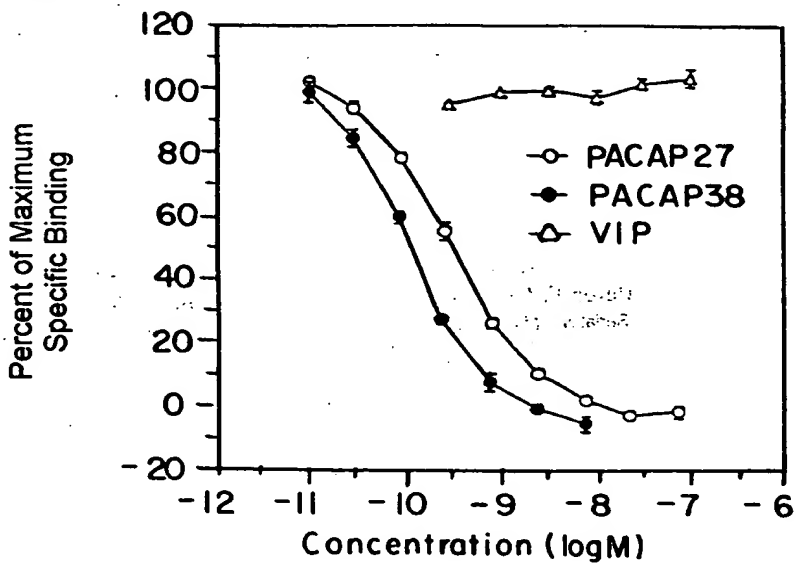


FIG. 36

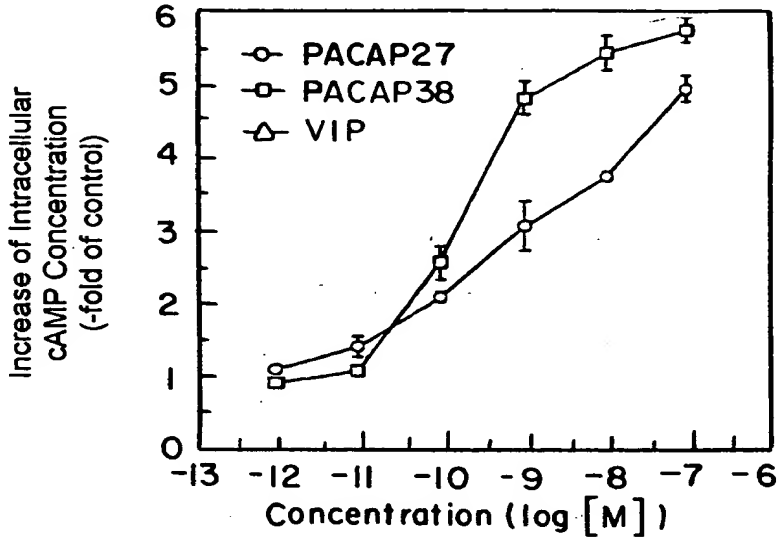


FIG. 37

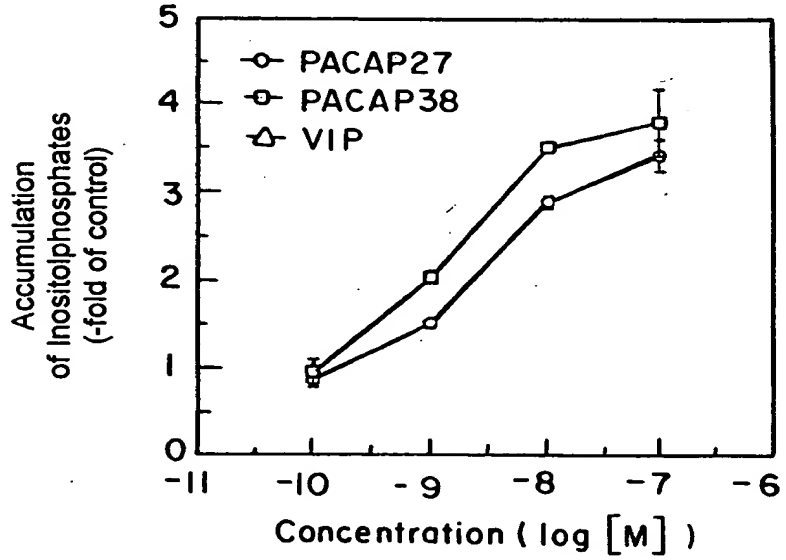


FIG. 32

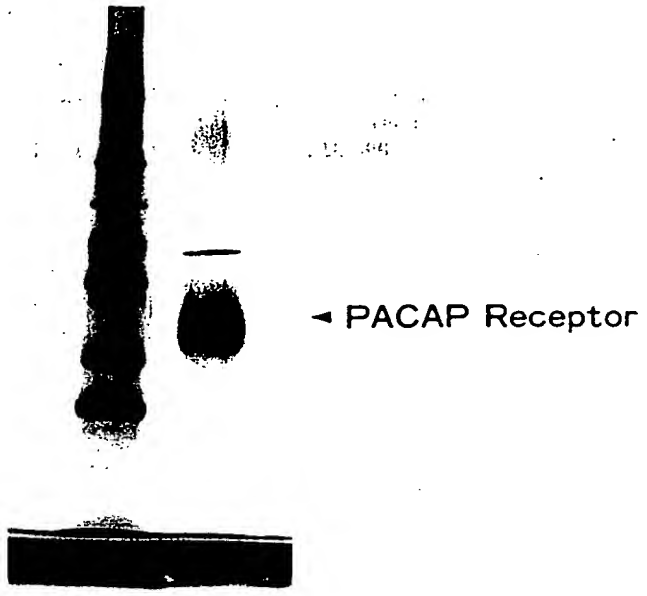

PACAP Receptor

FIG. 38

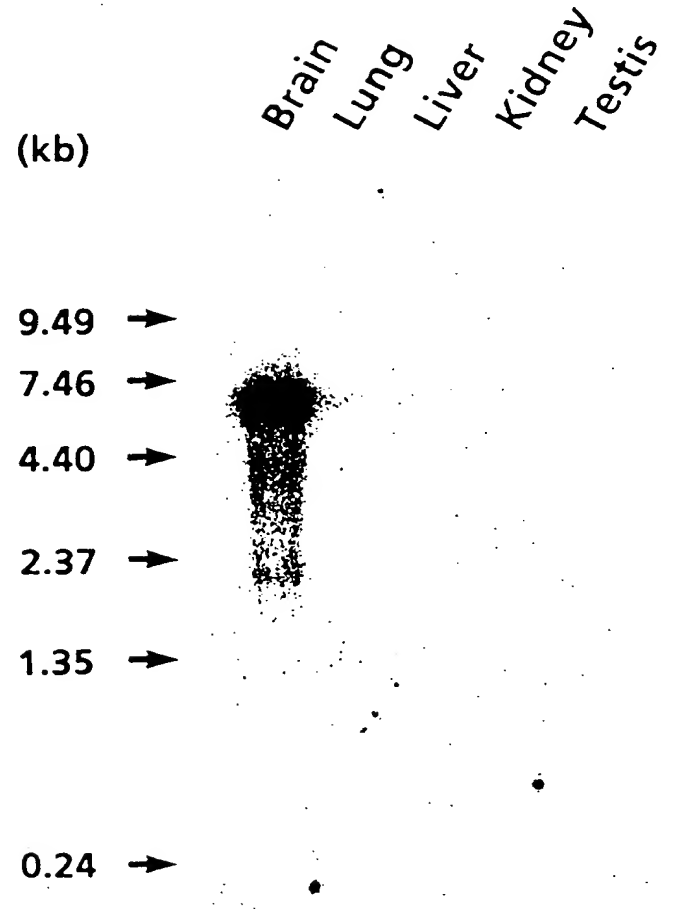

Brain
Lung
Liver
Kidney
Testis
(kb)
9.49
7.46
4.40
2.37
1.35
0.24

FIG.39

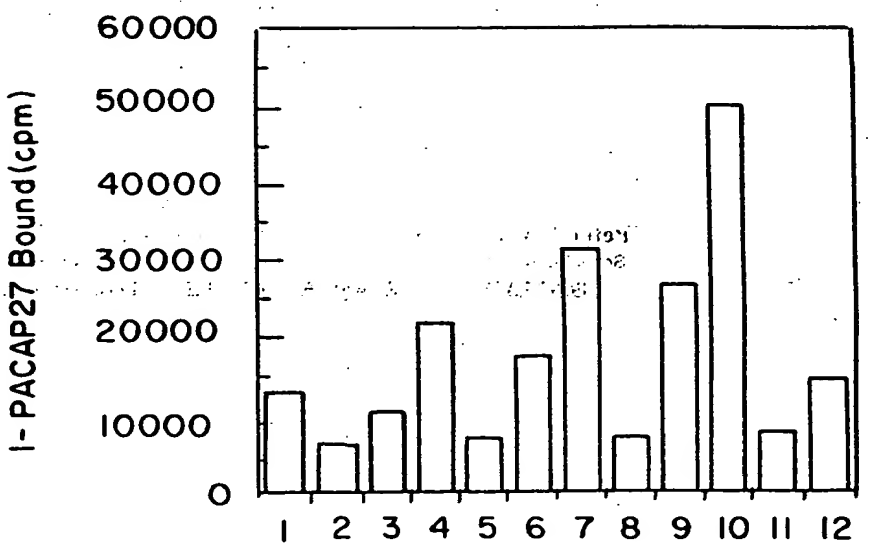


FIG.42

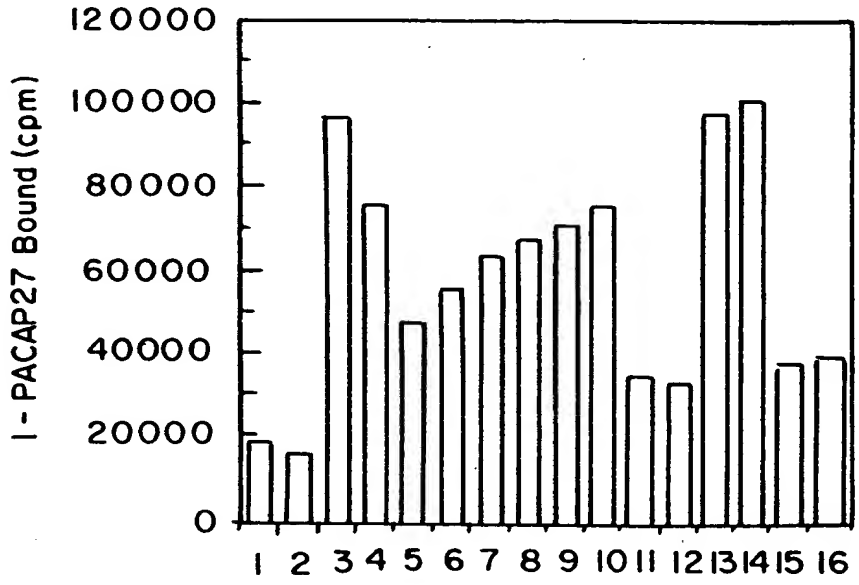
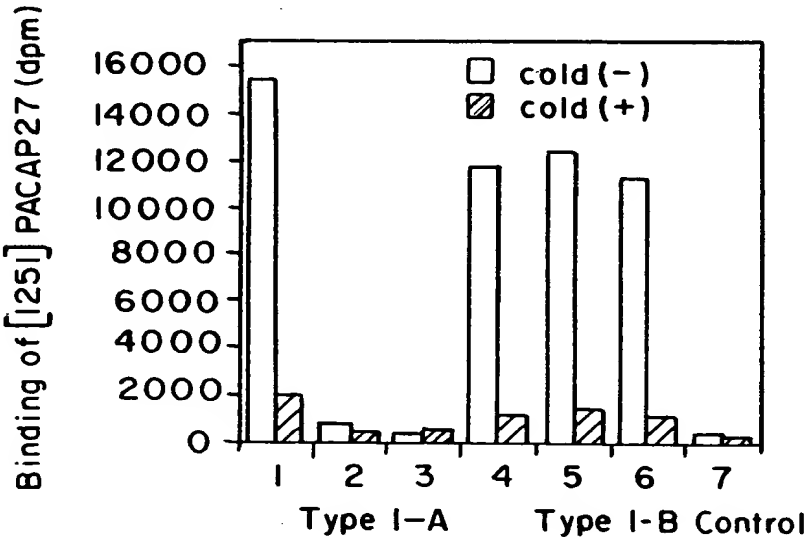


FIG.44



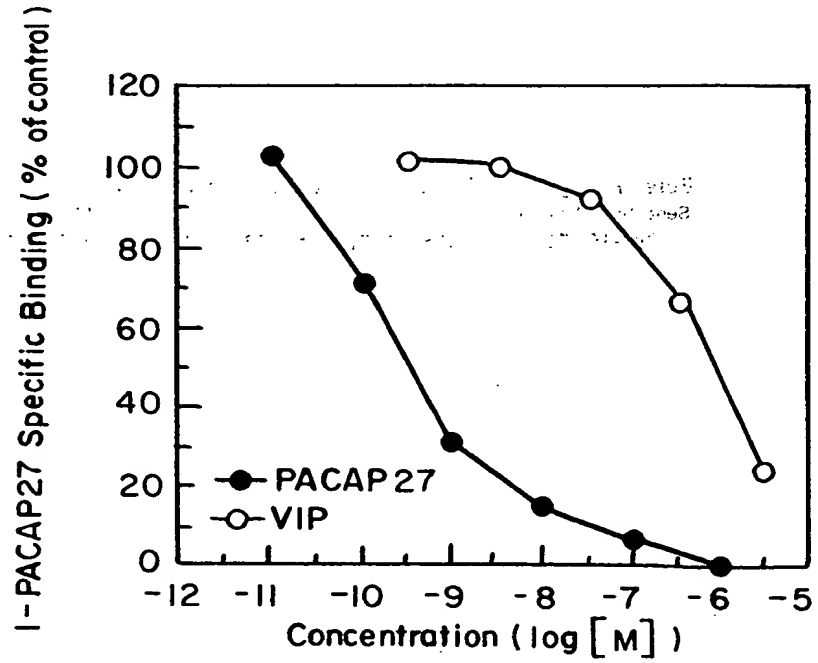


FIG. 40A

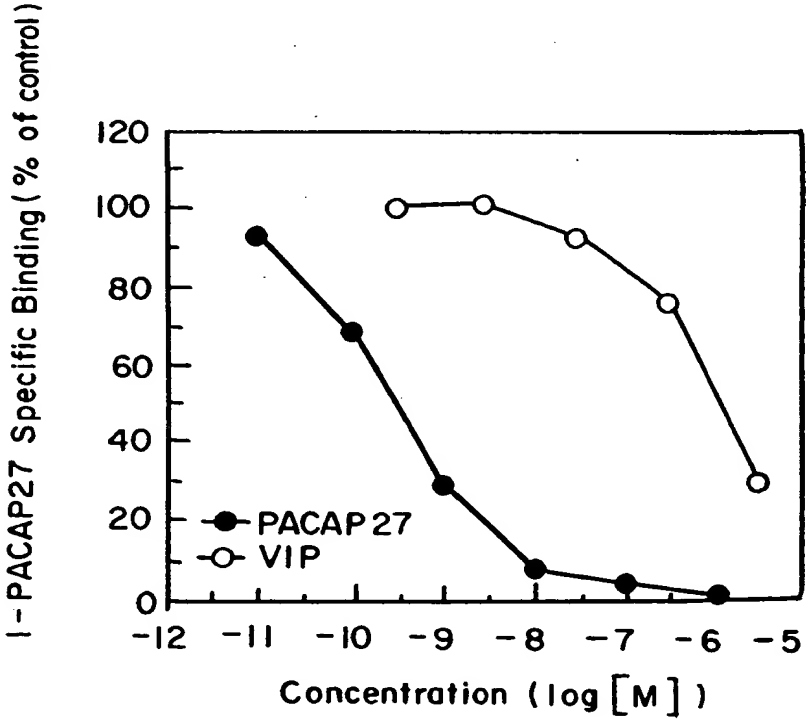


FIG. 40B

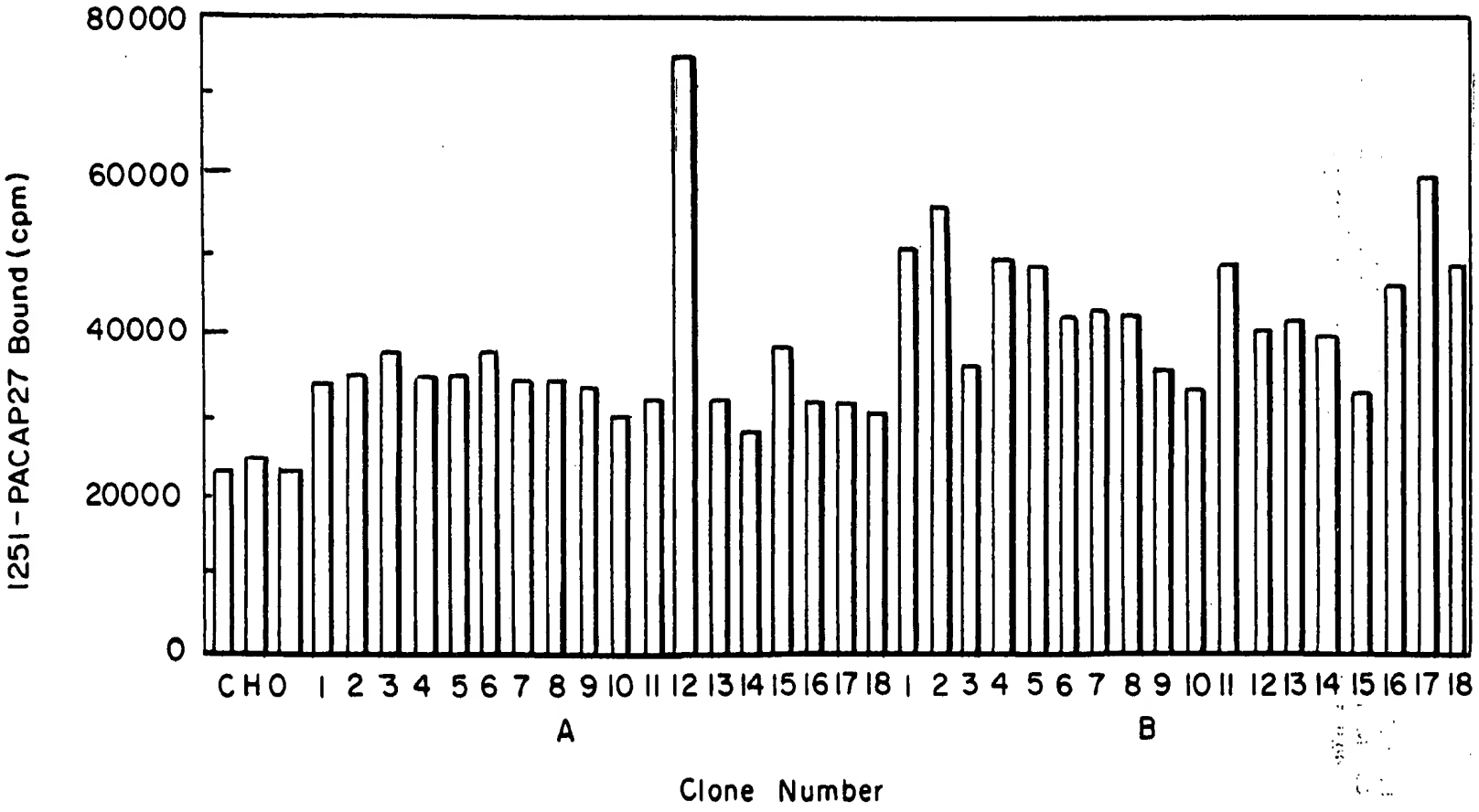


FIG. 41

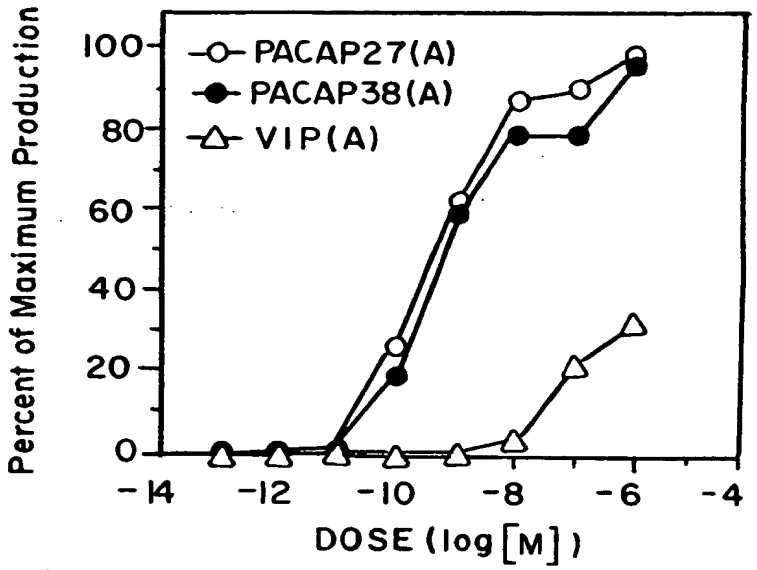


FIG. 43A

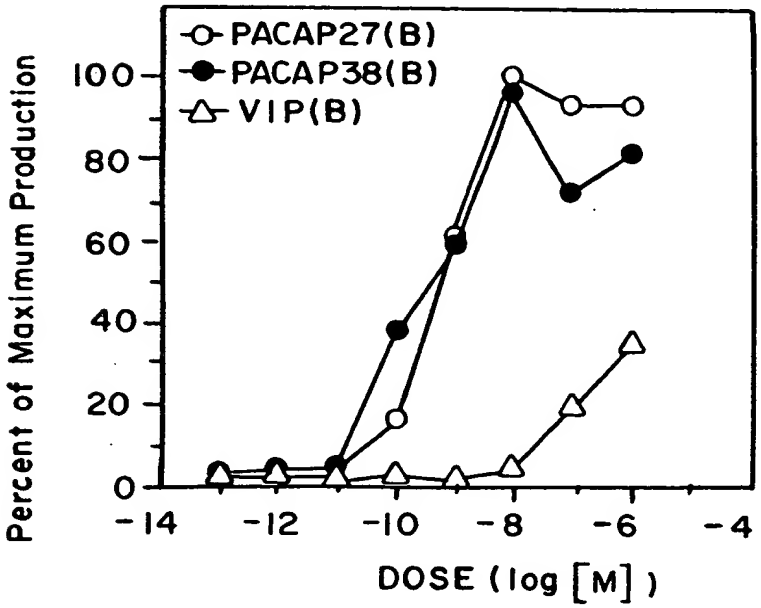


FIG. 43B

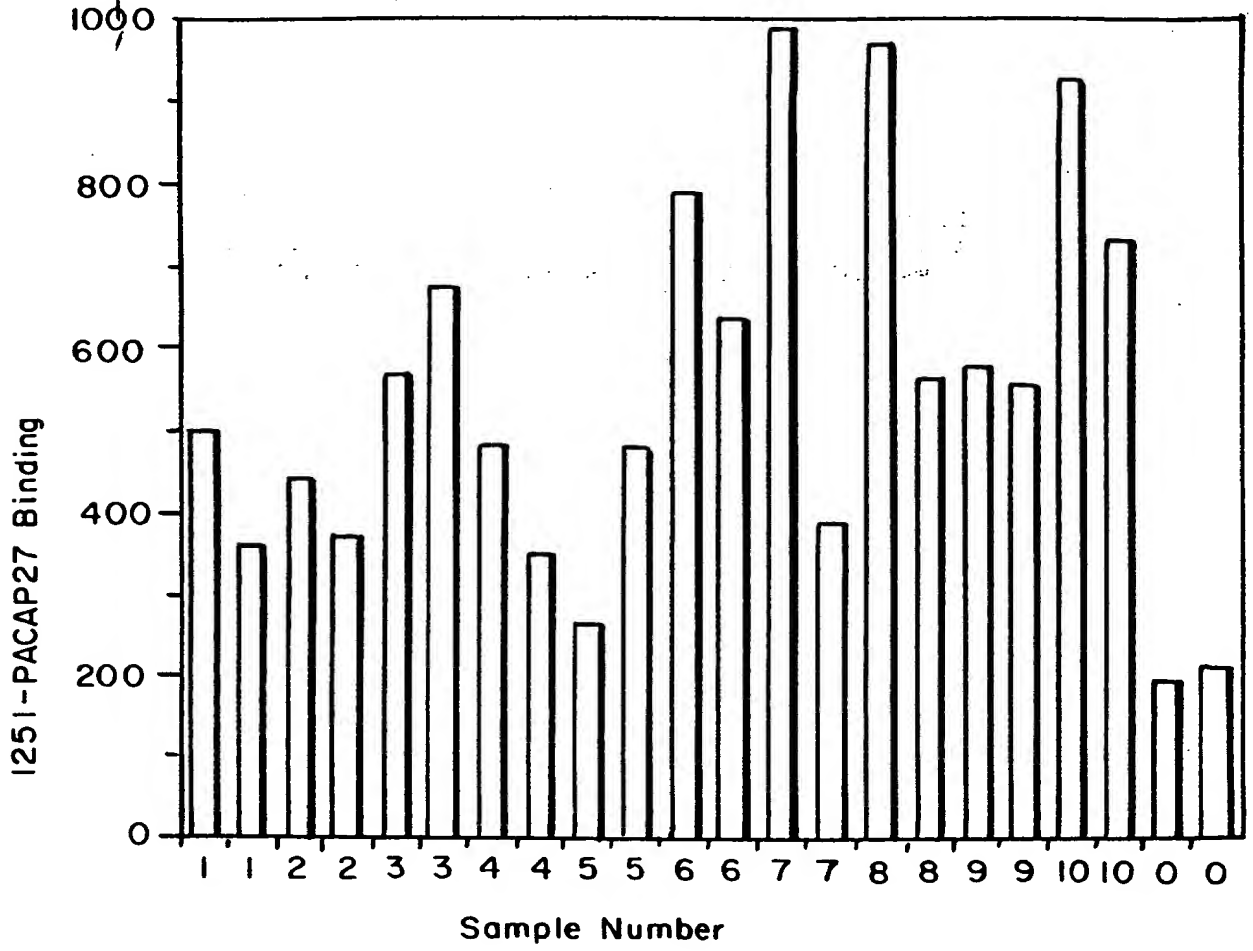

1000
800
600
400
200
0
1251-PACAP27 Binding
1 1 2 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 0 0
Sample Number

FIG. 45

FIG. 46

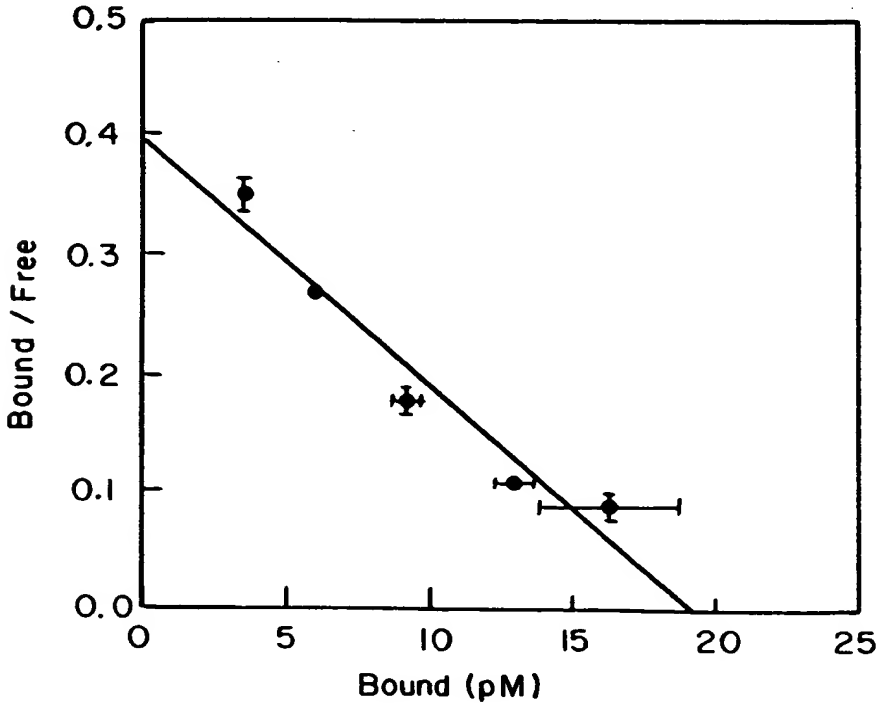

0.5
0.4
0.3
0.2
0.1
0.0
Bound / Free
0
5
10
15
20
25
Bound (pM)

FIG.47

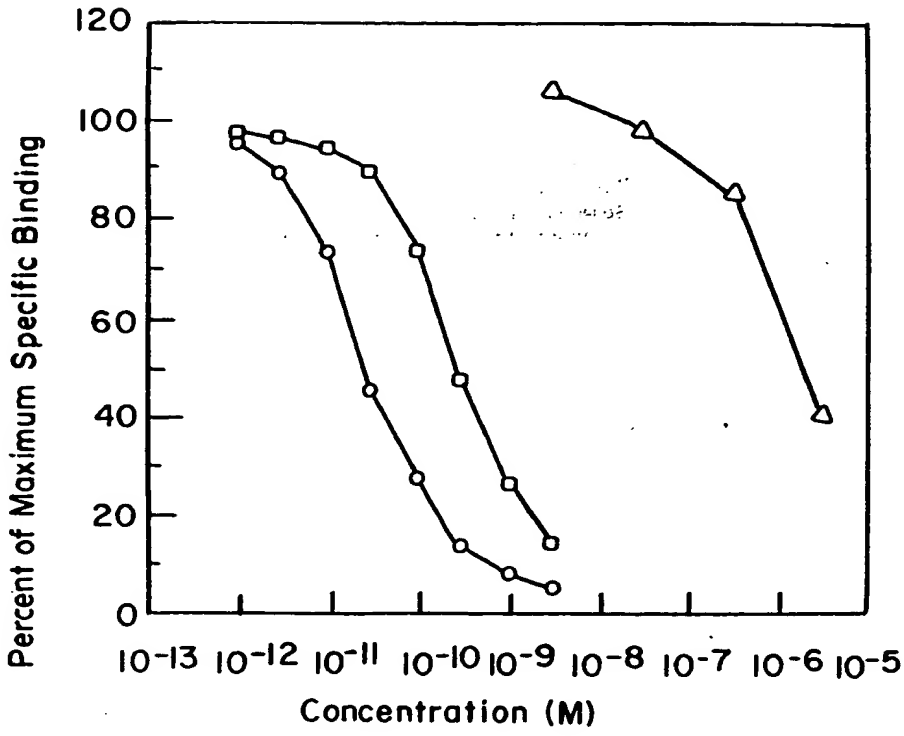
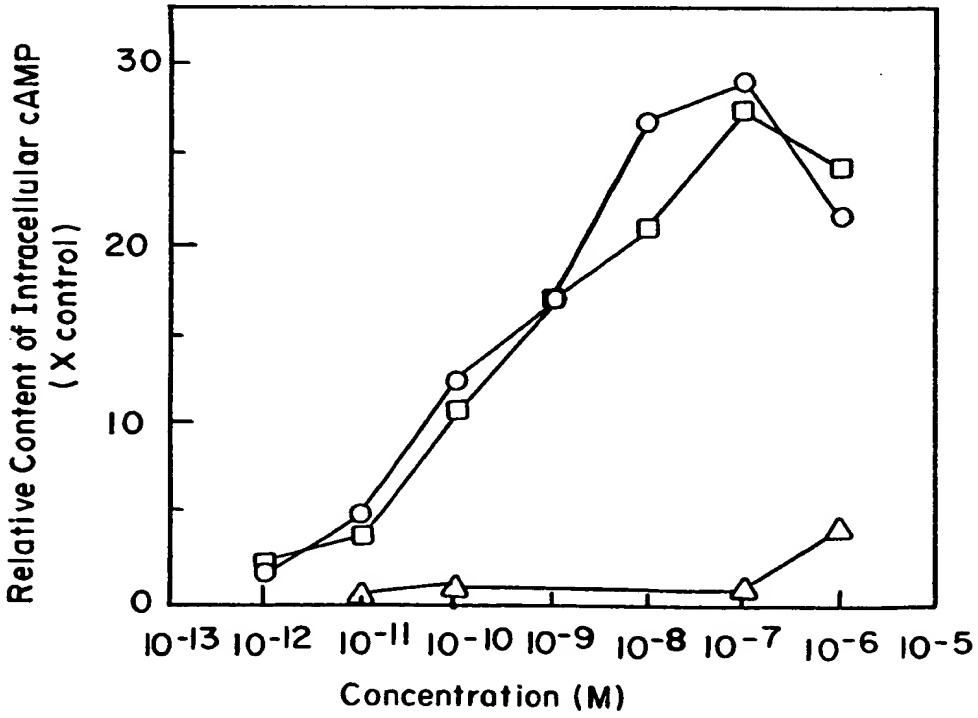

120
100
80
60
40
20
0
Percent of Maximum Specific Binding
10-13 10-12 10-11 10-10 10-9 10-8 10-7 10-6 10-5
Concentration (M)

FIG.48


30
20
10
0
Relative Content of Intracellular cAMP
(X control)
10-13 10-12 10-11 10-10 10-9 10-8 10-7 10-6 10-5
Concentration (M)

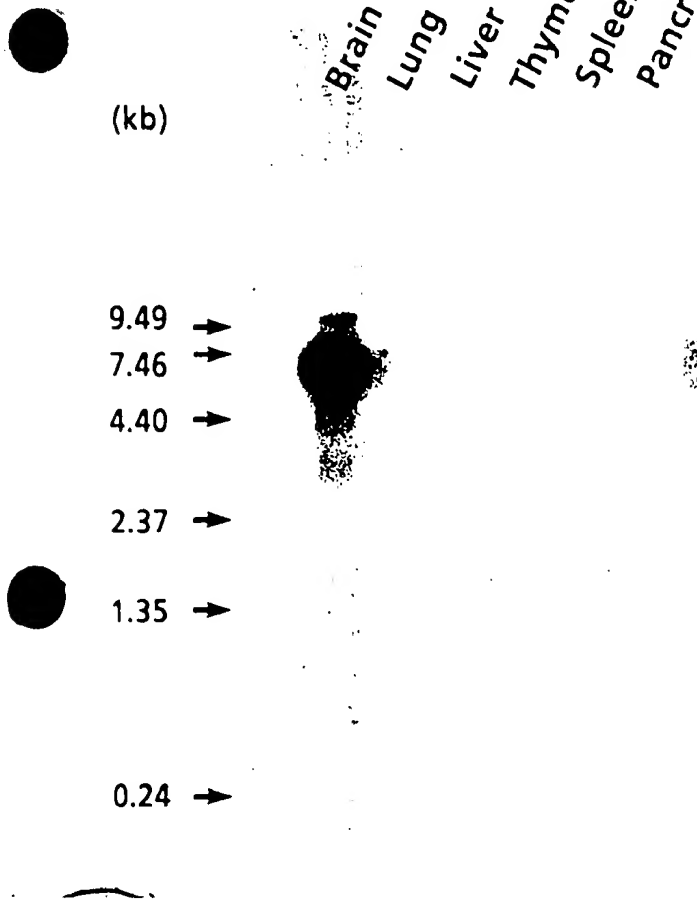

Brain
Lung
Liver
Thymus
Spleen
Pancreas
Placenta
(kb)
9.49
7.46
4.40
2.37
1.35
0.24

FIG. 49

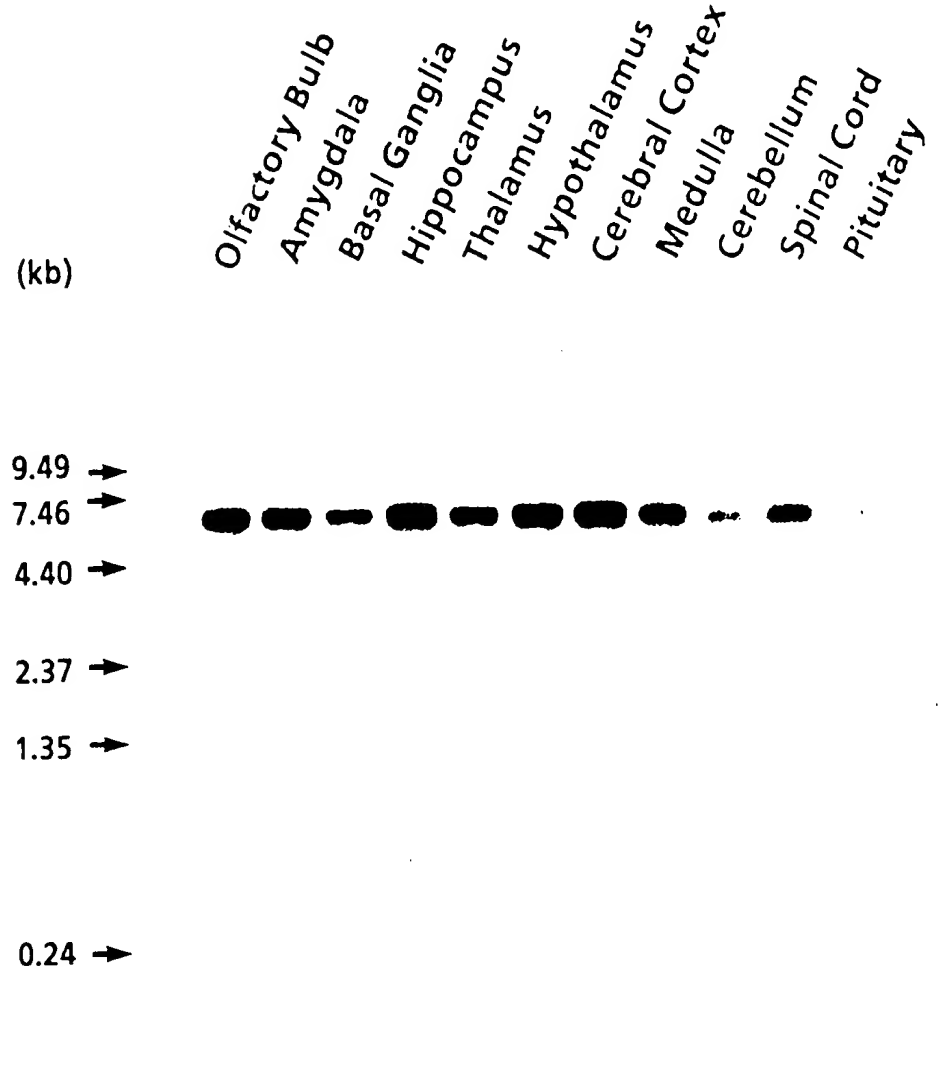

Olfactory Bulb
Amygdala
Basal Ganglia
Hippocampus
Thalamus
Hypothalamus
Cerebral Cortex
Medulla
Cerebellum
Spinal Cord
Pituitary
(kb)
9.49
7.46
4.40
2.37
1.35
0.24

FIG. 50

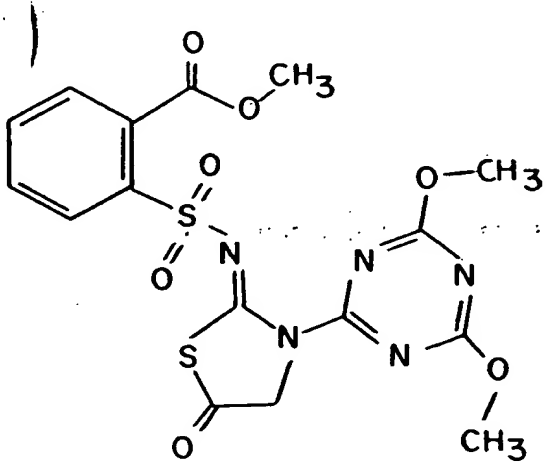


FIG. 51A

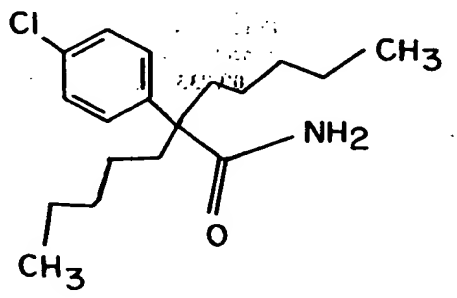


FIG. 51B

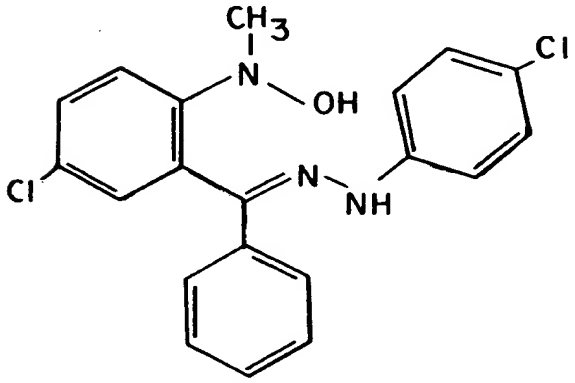


FIG. 51C

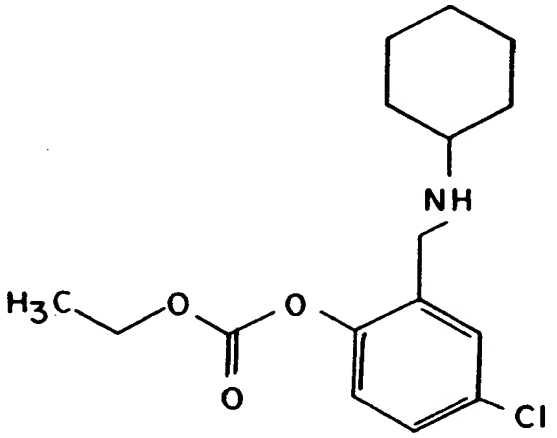


FIG. 51D

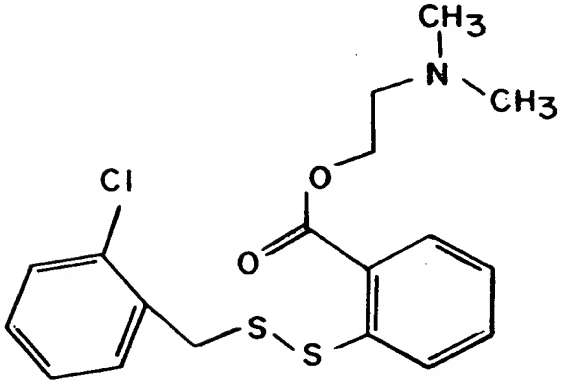


FIG. 51E

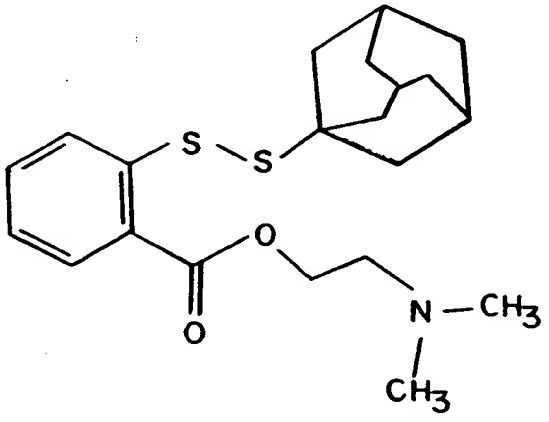


FIG. 51F

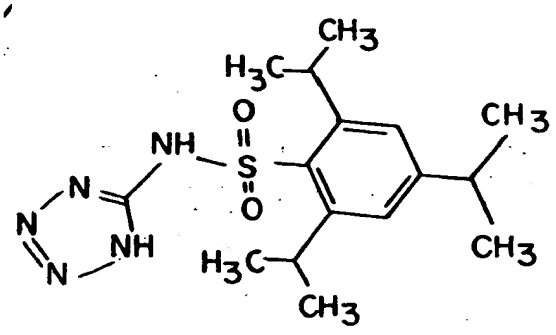


FIG.51G

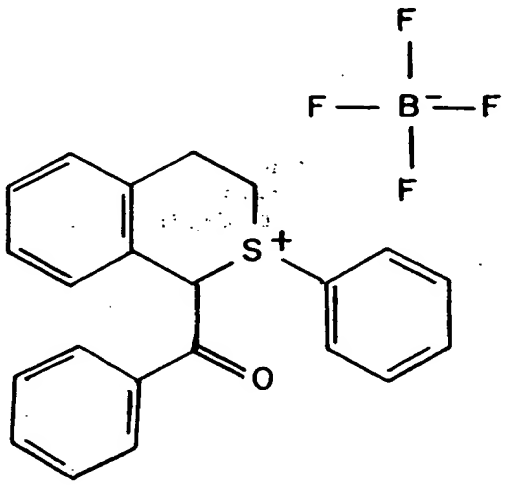


FIG.51H

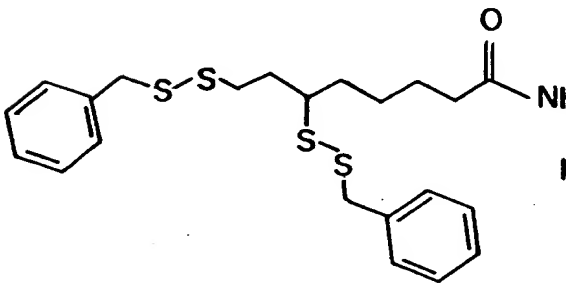


FIG.51I

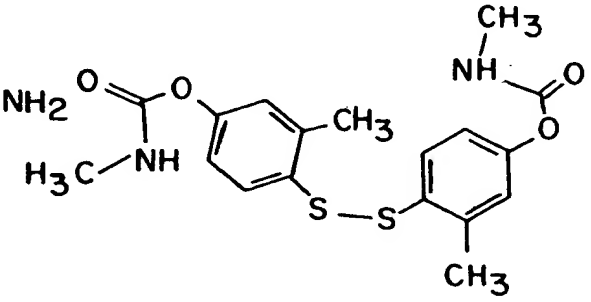


FIG.51J

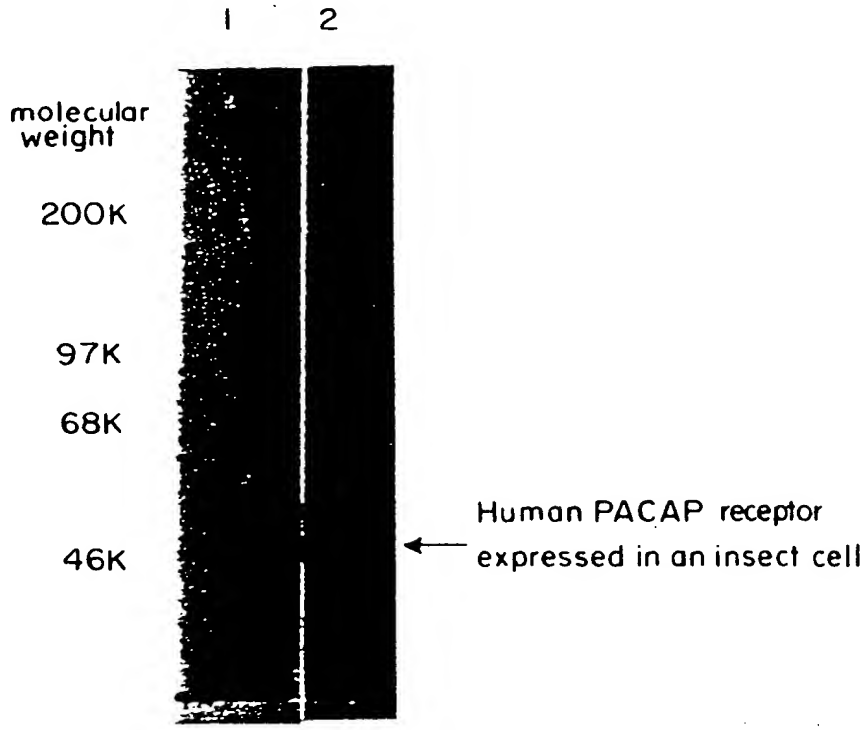

1
2
molecular weight
200K
97K
68K
46K
Human PACAP receptor expressed in an insect cell

FIG. 53

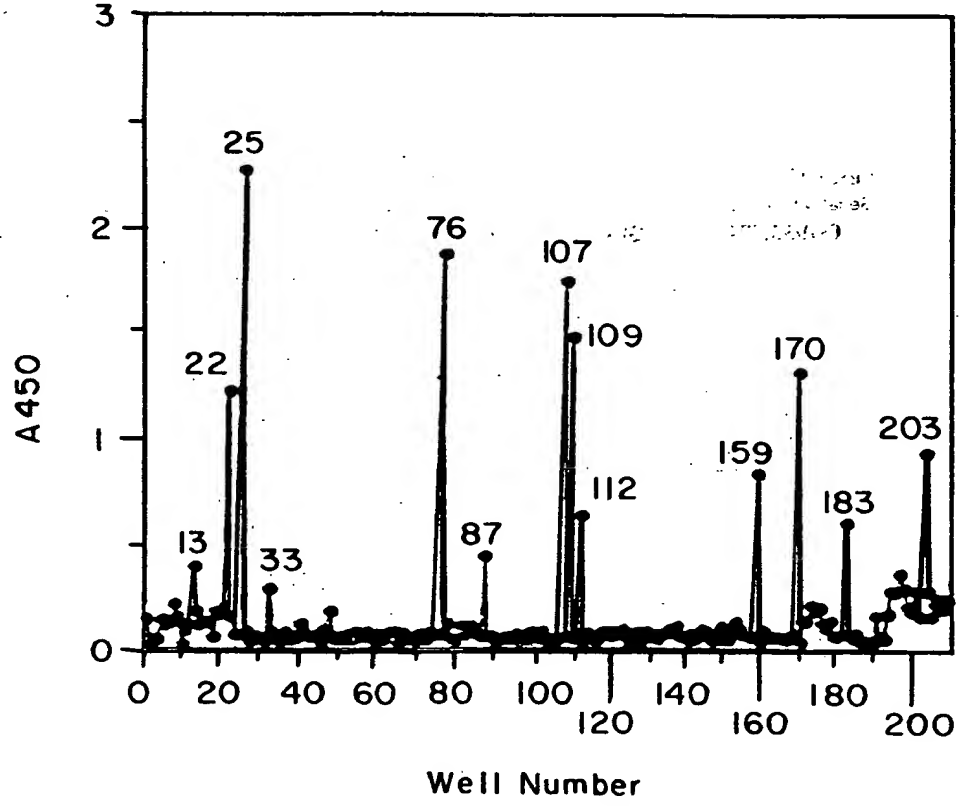

A450
Well Number
25
22
13
33
76
87
107
109
112
159
170
183
203
0
20
40
60
80
100
120
140
160
180
200
1
2
3

FIG. 52

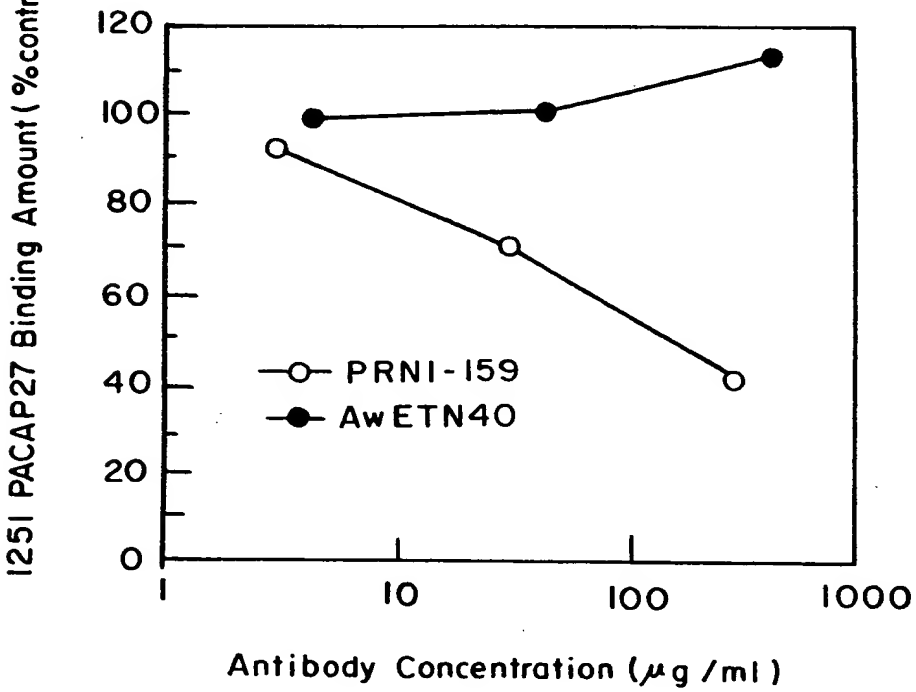

125I PACAP27 Binding Amount (%control)
Antibody Concentration (μg/ml)
PRNI-159
AwETN40
120
100
80
60
40
20
0
1
10
100
1000

FIG. 54